

STIC Search Report Biotech-Chem Library

STIC Database Tracking Number: 182281

TO: Phuong Bui

Location: REM/2A15/2C18

Art Unit: 1638

Friday, March 17, 2006

Case Serial Number: 09/938294

From: Barb O'Bryen

Location: Biotech-Chem Library

Remsen 1a69

Phone: 571-272-2518

poB

barbara.obryen@uspto.gov

Search Notes

RUSH



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Continuation (24 o
AC122149 Oryza sat
AL669987 Neurospor
AB026653 Arabidops
AR099685 Oryza sat
AF128457 Oryza sat
AF11922 Oryza sat
AF11269 Oryza sat
AF161269 Oryza sat
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AF161264 Lotus cor
AF166144 Lotus cor
AC1648577 Taeniopyg
Continuation (10 o
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AC152796 Bos tauru
AL939111 Streptomy
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AL684743 Penicilli
AK120574 Oryza sat
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Laid, J. Dey, N., Kim, C.-S., Bharti, A.K., Rudd, S., Mayer, K.F.X.,
Larkins, B., Becraft, P. and Messing, J.
Direct Submission
Submitted (27-027-2004) Waksman Institute, Rutgers University, 190
Frelinghuysen Rd, Piscataway, NJ 08854, USA
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bukaryophyta; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
 Arabidops
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AC023016 Arabido
AC023010 Homo sa
AK121451 Oryza s
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Lai,J., Dey,M., Kim,C.-S., Bharti,A.K., Rudd,S., Mayer,K.F.X., Lai,J., Dey,M., Eth,C.-S., Bharti,A.K., Rudd,S., Mayer,K.F.X., Characterization of the maize endosperm transcriptome and its comparison to the rice genome
Unpublished
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Pred. No. 2.1e-194;
); Mismatches 16;
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AP008209 023
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CR848712
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/mol_type="mRNA"
/db_xref="taxon:4577"
/clone="EL01N0367F09.c"
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SC0939111
AC152789
PM2D12B
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Matches 1058;
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ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
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JOURNAL
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            GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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Listing first 45 summaries
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Score

Result No.

Post-processing:

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SGKRCSREKEDNSDIKIQSVSGSLNPLEFMKSKLVLLVSHELSLSGGPLLLMELAFLL
SGYESEVWITTUQKPVEEDEVIKULEHMALDRGVQVISAKSGKAIDTALKSDLVVLNT
AVACKWLDAVLKDDVPKULPKVLMVIHEMREHYFKEDLVKKLLPFVAGAMIDSHATAEY
WKNRTHDRLGIKMPKTYVVHIGNSKELMEVAEDSFAKNVLREQVRESLGVRNEDILFG
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VQEMKLQKIVHFVNKTMKVAPYLAAIDVLVQNSQARGECFGRITIEAMAFKLPVLGTA
AGGTMBIVVNRTTGLLHNTGKDGVLPLAKNIVKLATNVKMRNTMGKKGYERVKEMFLE
URL:http://rarge.gsc.riken.jp/, Tel:81-45-503-9625,
Pax:81-45-503-9566)
An Ababidopsis full-length cDNA library was constructed essentially as reported previously (Seki et al. (1998) Plant J. 15:707-720; Seki et al. (2002) Science 296:141-145). cDNA cleaved with BamHI and XhoI was ligated to modified Lambda FLC-1-E vector (Carninci et al. (2001) Genomics 77:79-90) digested with BamHI and SalI. This clone is in a modified Bluescript vector.
Please visit our web site (http://rarge.gsc.riken.jp/) for further
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 translation="MAKPSTSMWATLQKKRWPLMILLVLSVSTVGMILVRSTFDSCSV
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Pred. No. 1.5e-110;
); Mismatches 371;
                                                                                                                                                                                                                                                                                           Organism="Arabidopsis thaliana"
mol_type="mRNA"
db_xref="taxon:3702"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /codon_start=1
/product="hypothetical protein"
/protein_id="RAD44016.1"
/db_xref="GI:51970668"
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                                                                                                                                                                                                                                                                                                                                                                                                                                            'note="common name: thale
                                                                                                                                                                                                                                                                                                                                                                                          clone="RAFL23-16-P14"
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                                                                                                                                                                                                                                                                                                                                                                                                                   ecotype="Columbia"
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Closki, Y., Seki, M., Ishida, J., Nakajima, M., Enju, A., Kamiya, A.,
Natusaka, M., Shin-i, T., Nakagawa, M., Sakamoto, N., Oishi, K.,
Kohara, Y., Kobayashi, M., Toyoda, A., Sakaki, Y., Sakurai, T., 'Iida, K.,
Akiyama, K., Satou, M., Toyoda, T., Konagaya, A., Carninci, P.,
Kawai, J., Hayashizaki, Y. and Shinozaki, K.
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Large-scale analysis of RIKEN Arabidopsis full-length (RAFL) cDNAs Unpublished
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Submitted (06-SEP-2004) Motoaki Seki, RIKEN Genomic Sciences
Center; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa
230-0045, Japan (E-mail:mseki@gsc.riken.jp,
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FLI CDNA.
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Large-scale analysis of RIKEN Arabidopsis full-length (RAFL) CDNAs Unpublished 2 (Dases 1 to 1709) 2 (Dases 1 to 1709) 3 Totoki,Y., Seki,M., Ishida,J., Nakajima,M., Enju,A., Kamiya,A., Narusaka,M., Shin-i,T., Nakagawa,M., Sakamcto,N., Oishi,K., Kohayashi,M., Toyoda,A., Sakaki,Y., Sakurai,T., Iida,K., Akiyama,K., Satou,M., Toyoda,T., Konagaya,A., Carninci,P., Kawai,J., Hayashizaki,Y. and Shinozaki,K. Direct Submission Submitted (06-SEP-2004) Motoaki Seki, RIKEN Genomic Sciences Center; 1-7-2 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:meski@gsc.riken.jp.	URL:http://rarge.gsc.riken.jp/, Tel:81-45-503-9625, Fax:81-45-503-9686) An Arabidopsis full-length cDNA library was constructed essentially as reported previously (Seki et al. (1998) Plant J. 15:707-720; Seki et al. (2002) Science 296:1141-145). cDNA cleaved with BamHil and XhoI was ligated to modified Lambda FLC-1-E vector (Carninci et al. (2001) Genomics 77:79-90) digested with BamHI and SalI. This clone is in a modified pBluescript vector. Please visit our web site (http://rarge.gsc.riken.jp/) for further details.	<u>Φ</u>	/ Godon start=1 /product="hypothetical protein" /product="hypothetical protein" /product="hypothetical protein" /product="hypothetical protein" /db_xxef="d1:5197062" /tranalation="makPSTSMWATLQKKRWPLMILLVLSVSTVGMILVRSTFDSCSV /tranalation="makPSTSMWATLQKKRWPLMILLVLSVSTVGMILVRSTFDSCSV /cranalation="makPSTSMWATLQKKRWPLMILLVLSVSTVGMILVRSTFDSCSV /tranalation="makPSTSMWATLQKKRWPLMILLVGSELSGCPLILMELAFLL RCVESEVVWITNORPVEDEVIKVLERVLENBERGHYFRPDIJVKHLPPVAGAMIDSHATAEY AVAGKMILDAJLKONVPRYTVVHLGNSKELMEVAEDSFAKOVLREQVRESLGVRNEDILFG IINNSVRGKGQDILFLRAFHESLKVIKETKKLEVPTMHAVVVGSNAAQTRETELANF VQEMKLQKIVHPVRTMKVAPYLAAIDVLVQNSQARGECFGRITIEAMAFKLPVLGTA AGGTMETVVNRTMYGROCYLPLARAIOTAMINTAMINTKGRSFKLPVLGTA HMMSHRIASVLREVLQHAKIHSRTTNSDH"	Match
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Qy 746 AATACAGATGCCACAAACTTATGTTGTTCACCTGGGGAATAGTAAAGAACTAATGGAAGT 805 Db 769 GATTAAAATGCCTAAAACTTATGTCGTGCACCTAGGAAATAGCAGAAGTTGATGGAAGT 828 Qy 806 TGCTGAAGACAATGTCGCAAGAAGAGCCTACGGGAACATTCGTGAATCCCTTGGAGT 865 Db 829 AGCTGAAGATATTCGCCAAGAATCTTCCGCTGAAGAAGTCTCTTGGAGT 886 Qy 866 ACGGAAGAAGACTCCTGTTTGCAATAATAAAAAGTGTATCACGAGAAAAGGCCAAGA 925 Db 889 GAGGAATGAAGACATACTATTTGCAATATTATTATTATTATTATTATTATTATTATTATTATT			1249 CTTGGGGCTGCT 1283 CCATCCTGCTGGC 1309 CCACCACACTGCTGG 1343 CCACCCCGGCGGCAC 1 1 1 1 1 1 1 1 1 1	OY 1463 ACAGAGCACTC 1474 Db 1489 AAAATTCACTC 1500 RESULT 4 AK176210 LOCUS AK176210 AK17621

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Arabidopsis thaliana (thale cress)
Arabidopsis thaliana
Arabidopsis thaliana
Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids II; Brassicales; Brassicacee; Arabidopsis.

I (bases I to 1763)
Yamada, K., Dale, J.M., Hsuan, V.W., Onodera, C.S., Quach, H.,
Toriumi, M., Wong, C., Wu, H.C., Yu, G., Yuan, S., Carninci, P., Chen, H.,
Kim, C.J., Narusaka, M., Nayuen, M., Palm, C.J., Sakuri, J.,
Seki, M., Shinn, P., Southwick, A., Tripp, M.G., Wu, T., Shinozaki, K.,
Arabidopsis Full Length cDNA Clones
L Unpublished
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Tortluni, M., Wong, C., Wu, H. C., Yu, G., Yuan, S., Carninci, P., Chen, H.,
Cheuk, R., Hayashizati, Y., Ishida, J., Jones, T., Kamiya, A., Kawai, J.,
Kim, C.J., Narusaka, M., Nguyen, M., Palm, C.J., Sakurai, T., Satou, M.,
Seki, M., Shinn, P., Southwick, A., Tripp, M.G., Wu, T., Shinozaki, K.,
Davis, R.W., Ecker, J.R. and Theologis, A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The Salk, Stanford, PGEC (SSP) Consortium members carried out the sequencing and annotation of the RAFL cDNAs: Yamada,K., Dale,J.M. Hsuan,Y.W., Onodera,C.S., Quach,H.L., Toriumi,M., Wong,C., W.W., C., Yu.G., Yuan,S., Chen,H., Cheuk,R., Jones,T., Kim,C.J., Nguyen,M., Palm,C.J., Shinn,P., Southwick,A., Tripp,M.G., Wu,T., Davis,R.W., Ecker,J.R. and Theologis,A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               collection and clustering of RAFL CDNAS (RAFL CDNA: 'RIKEN Arabidopsis Full-Length CDNA': Seki,M., Narusaka,M., Ishida,J., Satucu,M., Kamiya,A., Sakural T., Carninci,P., Kawai,J., Hayashizaki,Y. and Shinozaki,K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (16 MAY-2003) Plant Gene Expression Center, 800 B. Street, Albany, CA 94710, USA
RIKEN Genomic Sciences Center (GSC) members carried out the
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                         cccretrcreaagarcarctrccraaggrccrrccgaagarrrrgrggarccarga
                                                                    recaditicicaagacaarericciaaagircritciraaagiacricgegaaricarea
                                                                                                                                                                   GATGAGAGGTCACTATTTCAAACCGGATTTAGTCAAGCACCTTCCGTTTGTTGCAGGTGC
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                                                                                                                                                                                                                                                                                                                 746 AATACAGATGCCACAAACTTATGTTGTTCACCTGGGGAATAGTAAGAACTAATGGAAGT
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                                                                                                                    AATGCGTGGGCATTACTTTAAGGTTGAATATGTCAAACATCTTCCCTTTGTTGCTGGAGC
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TNQKPLEDDEVVYSLEHKMLDRGVQVISAKGQKAVDTSLKADLIVLNTAVAGKMLDAV
LKENVVKVLPKILWWIHEMRGHYFNADLVKHLPFVAGAMIDSHATAGYWKNRTQARLG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IKMPKTYVVHLGNSKELMEVAEDSVAKRVLREHVRESLGVRNEDLLFGI INSVSRGKG
ODDERARPHESLER IKEKKLQVPTMHAVVVGSDMSKGYTREFELENDVREKKLENFVH
PVNKTLITVAPY I AA DUVLOVOSQARGECFGR I TI EANAFKLPVLGTAAGGTKEI VVNG
TYGLLHSAGKEGVI PLAKNI VKLATQVELRLRMGKNGYERVKEMFLEHHMSHR I ASVL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /trānslation="MVKASTMQRKRWALMVLLPLSVSTVCMILVRSSFETCSISSQFV
EEKNGESSAAKFQSNPLDFMKSKLVLLVSHELSLSGGPLLLMELAFLLRGVGADVVWI
ed equally
(SSP/PGEC)
                                                                                                                                                                                                                                                                                                                                                                         pBluescript vector2
                                                                                                                 Annotation based on July 2002 version of the Arabidopsis
  (SSP/PGEC) and Seki, M. (RIKEN GSC) contributed to Shinozaki, K. (RIKEN GSC) and Theologis, A.
                                                                                                                                                                                                                                                                                                                                                                                          /note="This clone is in a modified (lambda PS) as a BamHI/XhoI insert.
                                                    contributed equally to this work as PIs.
                                                                                                                                                                                                                             thaliana"
                                                                                                                                                                                                                                                                                                                                         clone="RAFL21-18-G06 (R51064)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /evidence=experimental
/product="unknown protein"
/protein_id="AAP40442.1"
/db_xref="G1:30793985"
                                                                                                                                                                                                                          /organism="Arabidopsis
/mol_type="mRNA"
/db_xref="taxon:3702"
/chromosome="1"
                                                                                                                                                                Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                   ecotype="Columbia"
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/gene="At1g75420"
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|gene="At1g75420"
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                                                                                                                                              submitted to Genbank
                             chis work.
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BT008621 1765 bp mRNA linear PLN 16-MAY-2003 Arabidopsis thaliana clone RAFL21-18-G06 (R51064) unknown protein (Al1975420) mRNA, complete cds.

GI:30793984

BT008621.1

ACCESSION VERSION

RESULT 5 BT008621 LOCUS DEFINITION

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Arabidopsis thaliana chromosome I BAC F14P1 genomic sequence,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Arabidopsis thaliana (Liaze Cress)
Arabidopsis thaliana
Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Bermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosida; eurosida II; Brassicales; Brassicaceae; Arabidopsis.

1 (bases 1 to 90341)
Altafi,N., Palm,C.J., Conway,A.B., Conn,L., Hansen,N.F.,
Altafi,H., Nguyen,M., Lam,B., Southwick,A., Miranda,M., Brooks,S.,
Buehler,B., Johnson-Hopson,C., Khan,S., Kim,C., Koo,T., Lee,J.M.,
Lenz,C., Liu,A., Liu,S., Mukharsky,N., Pham,P., Sakano,H.,
Shinn,P., Toriumi,M., Vaysberg,M., Yu,G., Ecker,J., Theologis,A.,
and Davis,R.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Direct Submission
Submitted (01-MAR-2000) DNA Sequencing and Technology Center,
Stanford University, 855 California Avenue, Palo Alto, CA 94304,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Center,
CA 94304,
                                                                                                                                                                                                                                                                                                                                                                                        1486 GGAACATCATATGTCACATCGAATAGCTTCGGTACTCAAAGAAGTCTTGCAACACGCAAA
CCGTGGAGAATGCTTTGGAAGGATAACAATTGAAGCAATGGCATTCAAGTTGCCAGTATT
                                                                                                                                                                                                                                                                                                                                                      1406 GGAGCACCACATGGCTGAGGATCGCGGCGGTGTTGAAGGATGTCCTGAGGAAATCACA
                                                                                                                 TCCTGCTGGGAAGGAGGCGTGTGCTTGCAAAGAACATCGTCAGACTCGCAAGCA
                                                                                                                                                                                                    Federspiel, N.A., Palm, C.J., Conway, A.B., Conn, L., Hansen, N.F.,
                         CAGAGAGAATATGGGAGAATAACAATCGAAGCCATGGCCTTTAAGCTACCTGTACT
                                                                                     GGGCACGGCTGCTGGAGGGACCACGGAGATCGTCCTGGACGGCTCGACTGGCCTTCTGCA
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Submitted (09-MAR-2000)
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AC024609
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JOURNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   525
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TGCTGAAGACAATGTCGCAAGAAGAGTCCTACGGGAACATATTCGTGAATCCCTTGGAGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1006 rergricereceageerrecacgaaagrerrgaaagaardaaagagaagaadaacrreaggr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GCCTAGAATACATGCTGTAGTTGTGGGAAGTGATGTTAATGCTCAGACCAAATTTGAGAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cerreirricearcacraarcaaageceaerreaagargargargargrerraraga
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GCATAGGATGTTGAACCATGGAGTGCAGGTTTTACCAGCTAGAGGACAGGAGCCAGTTGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AATACAGATGCCACAAACTTATGTTGTTCACCTGGGGAATAGTAAAGAACTAATGGAAGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                886 AGCTGAAGATAGTGTTGCCAAGAGAGTTCTCCGTGAGCACGTCCGAGAATCTCTTGGAGT
                                                                                                                                                                                                                                                                                                                                                                                                             526 ACACAAGATGTTGGATCGAGGATTCAGGTTATCTCTGCAAAGGGTCAGAAAGCTGTAGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CCCTGTTCTGAAAGATCATGTTCCTAAAGTCCTTCCGAAGATTTTTGTGGTGGATCCATGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GATGAGAGACACTATTCAATGCTGATTTGGTCAAACACCTCCCTTTTGTTGCAGGGG
                                                                                                                                                                                                                                                                                              266 GAGICCCCTCGGGIICAIGAGGICCAAGCICGIGCICCTCGICCCAIGAGCICTCCCI
                                                                                                                                                                                                                                                                                                                        AGTGGTGTGGATAACAAACCAGAGATCACAAGAAACAAATGATGTCACATATAGCTTGGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TATTECTCTAAAAGCTGATCTGGTTATCTTAAACACTGCTGTTGCTGGCAAGTGGCTTGA
                                                                                                                                                                                                                                                    Gaps
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                                                                                                                                                                                                         DB 15; Length 1765
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                                                                                                                     sequence"
                                                                                                                                                                                                                                                  0, Mismatches 382;
                                                                                                                                                                                                                             Pred. No. 3.1e-108
                                                                                                                   genomic
                                                                                                                                                                                                    tch 34.7%; Score 590.8; al Similarity 68.2%; Pred. No. 3.16 820; Conservative 0; Mismatches
                                                                                          /gene="At1g75420"
/note="compared to
/replace="t"
                         1565. .1765
/gene="At1g75420"
1749
      KEVLQHAKARALR"
                                                                         misc difference
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Best Local S
Matches 820
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oin(70742. .70816,70957. .71382,72084. .72173,72904. .73284)
gene="F14P1.3"
note="Hypothetical protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                |oin(74552, .74694,74769, .75090,75300, .75449,75558, .75735,75908, .75987,76159, .76245,76328, .76417
                                                                                                                                                                                                                                                                                                                        MSNSEISSIGIADLGCSSGPNSLLSISNIVDTIHNLCPÖLDRPVPELRVSLNDLPSND
FNYICASLEBFYDRVNNKEGLGFGRGGESCFVSAVPGSFYGRLFPRRSLHFVHSSS
SLHWLSQKITGSHNRRELLSMGTPSSSYVHGQRGIVGITEEEKIDAFNAPYYAASSE
ELKKVVIEKGSFSIIDKLEISPIDMEGGSISEESYDLVIRGKPEALASGRRVSNTIRAV
VEPMLEPTFGENVMDELFERYAKIVGEYFYVSSPRYAIVILSLVRAG"
                                                                                                                                                                                                                       protein id="AAF98406.1"
db_xref="GI:9795588"
/translation="MEVWRVLHMNKGNGETSYAKNSTAQSNIISLGRRVMDEALKKLM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MČKMLVSLEKEBELGSMQRDVGFVCEAMLAFPLNLPWTRFHKGIMARGRVMEMLEKII
RERRNEINSHNNHHEDFLQQLLAVDNDTPQLTDAEIKDNIITMIIAGDTTASALTWM
VKYLGENQKVLDIIIEEQSQITKKASNKPFLELEDLSEMPYASKMVKESLRMASVVPW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               80606. 80776
/gene="F14P1.6"
/notes="Similar to defensin, Similar to defensin AMP1 (anti
microbial protein)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STVTPFDSYNMSKFEDVGYYNNSTYRENVPAFQAVKAVEESSYSYDQEVVEMSSKSYR
RTSRSBKKWTTENTERVTKTGSMR&QSMOGLSSGEBFRRTITGTFVSBQKKM
RTSRSBKWDQLENYTHRASQUDDRVHYWEHGAVPQMQNDDVPQLONGSVPWWQNG
SVSQLAONSDVPQWQNGSYLQLQNGDVPQWQTGGVSQLAONGYHEPQNGIVQWKGSRDDG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        translation="MMAVEGRICERRSKTWTGFCGNTRGCDSQCKRWERASHGACHAQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RRIRYGSCPRTSLFGETHVPLSTTESARLVLNNDSGMFTKRYIKSIGELVGDRSLLCA
PQHHHKILRSRLINLFSKRSTALMVRHFDELVVDALGGWEHRGTVVLLTDLLQITFKA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          complement(join(81552. .81800,81920. .82031,82136. .82233,82329. .82436,82543. .82581,82670. .82741,82820. .83068,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EDFTGSKMLVLRYAVLNLQVIQAAIRFAKQEGLSVSLDLASFEWKRNSKSELRQLLES
GNIDLCFANEDEAAELLRGEQEAGPEAALEFLGRHCRWAVVTLGSKGCIAKHDKEVVH
ISAIGETVATDATGAGDLFASGFLYGLIKGLSLEECCKVGSCSGGSVIRALGGEVTPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        translation="MFQDRKKSTAGVPPGSDGFPVIGETLQFMLSVNSGKGFYEFVRS"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /trānslation="meaekaeaswiyenifonckyivgisavvafgyccipvivnqih
GFFIWFDWFTLVLRNLFFISVVVSIIIFLIYVIFSKIQTTEKKEPDLYDQYVAAVPPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             translation="MVAEALPKCPEAPLVLGLQPAALIDNVAPVDWSLLDQIPGDRGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SIAVQKDELEHMLKELDAHISVAPLKKMAGGSVTNTVRGLSVGFGVATGIIGAYGDDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             QGQLFVSNMGFSGVSISRLRKKKGSTAQCVCLVDDSGNRTMRPCLSSAVKIQADELSK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 note="Hypothetical protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /gene="F14P1.5"
complement(77375. .78430)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      complement (77375. .78430)
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/proteIn_id="AAF98405.1"
/db_xref="GI:9795587"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        protein_id="AAF98402.1"
db_xref="GI:9795584"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        'protein_id="AAF98400.1"
'db_xref="GI:9795582"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               id="AAF98401.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            note="Unknown protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    note="Unknown protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             'db xref="GI:9795583
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SGRHRHRHGHRSRKHRQ"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FPRLVLQDCEMEGLL"
                              70742. .73284
/gene="F14P1.3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        gene="F14P1.4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 gene="F14P1.5"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        gene="F14P1.6"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  'gene="F14P1.7"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             codon start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 codon start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             30606. .80776
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FPGFACFCYFNC"
                                        gene
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         e-mail for correspondence: arab@sequence.stanford.edu
Genes with similarity to proteins in the databases are named
'putative', "like' or 'similar to'. Genes that have EST
similarity but no significant protein similarity are described as
'unknown proteins'. Genes that are annotated based only on gene
prediction software are described as 'hypothetical proteins'. The
gene prediction programs used to predict genes include: Grail
(Informatics Group, Oak Ridge National Laboratory,
http://compbio.ornl.gov/section/index.html), GENSCAN (Chris Burge,
http://gnomic.stanford.edu/-chris/GENSCAN html), and NetPlantGene
(S.M. Hebsgaard, et al., Cabris/GENSCAN html), and NetPlantGene
Location/Qualifiers
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      join(60210. .60507,60608. .60778,60878. .60927,61025. .61081,61184. .61249,61387. .61461,61599. .61717,61807. .61960)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 join(63540. .63596,63685. .63951,64046. .64123,64205. .64306,
64387. .64436,64527. .64626,64741. .64833,64927. .65040,
65139. .65253,65359. .65756)
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KSGPDGFMVKMKDGRQLRCVHNNPQGGNLPNYAPHSAIVLKMEDGTGLLLPIIVLEMP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SVI.LMAAMTUVQIARRTMYQVYKDMYDKMGYRVRI.VRVTTRVHBAYFAELYI.SKVGDK
SDCVSFDLRPSDAINIAVRCKVPIQVNKYLAYSDGMRVIDSGKI.SKQTPASDGIL.FTB
LDRPNGQPCFDTKEFDLVRNMQAVDERYDBAGKLSI.SHPPYLVVII.VLINY"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LDVQGLGLKNFTKTARDLIIQLQKIDSDNYPETLHRMFIINAGSGFKLLMGTVKSFLD
PKTVSKIHVLGNKYQNKLLEMIDASQLPDFFGGTCTCADQGGCMRSDKGPWKDSEILK
MGRSGGTFCRHAGAFLSSDSQISSSDKPTYSLKVSDTSTAKSGSELEEMASPKTNTNN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HVPKLTPVSEYANGNISPTVLSEYEECVPMVDKVVDVAWQLQEMPNASEGPQYTSSLG
KIGSVRHIWSWLTAFPISFFTLLASLALPQTKEHSQLHSSSVRAELCDERIARESRPP
SPPRSTITERVIISSVLSRLGDLEKQIENLHSRKSEMPHEKEELLNAAVYRVDALEAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 translation="MWTNMIQWRRDFGTDTILEDFEFPELDEVLRYYPQGYHGVDKEG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    'translation="MRSLQAPVVCPSVRPRQLGVSALLVNCSVSKTRSLRKQFWGNQT"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RPVYIERLGKVDASKLMQVTTLERYLRYHVKEFEKTITVKFPACCIAAKRHIDSSTTI
Altafi,H., Nguyen,M., Lam,B., Southwick,A., Ecker,J., Theologis,A.
and Davis,R.W.
Direct Submission
                                                                                                                                                                                                                       Pederspiel,N.A., Palm,C.J., Conway,A.B., Conn,L., Hansen,N.P.,
Altafi,H., Nguyen,M., Lam,B., Southwick,A., Ecker,J., Theologis,A.
and Davis,R.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /mol_type="genomic_DNA"
/db_xref="teaxon:3702"
/chromosome="1"
/clone="F14P1"
1. :9676
/note="worlap with IGF clone P6F9, gb|AC007797, see
GenBank record for BAC clone P6F9 for annotation in this
                                                                                                                                                                                                                                                                                                                     Direct Submission
Submitted (12-SEP-2000) DNA Sequencing and Technology Center,
Stanford University, 855 California Avenue, Palo Alto, CA 94304,
                                                                                              Submitted (11-AUG-2000) DNA Sequencing and Technology Center, Stanford University, 855 California Avenue, Palo Alto, CA 94304,
                                                                                                                                                                                                                                                                                                                                                                                                                                                     On Mar 9, 2000 this sequence version replaced gi:7121532.
Bases 1-59,676 of IGF clone F14P1 overlap with IGF clone F6F9,
gb|AC007797.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   organism="Arabidopsis thaliana"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    'note="Hypothetical protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /proteIn_id="AAF98407.1"
/db_xref="GI:9795589"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          protein_id="AAF98408.1"
db_xref="G1:9795590"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           'note="Unknown protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        gene="F14P1.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   gene="F14P1.1"
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60210. .61
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FPRARLLEMGYKNPVLLIHPLGGFTKADDVPLDVRMEGHSKVLEDGYLDPKTTIVSIFP
SPRHYAGPFTSVQWHAKARI NDGANFYIVGRDPAGMGHPTEKRDLYDPHGKRVLSMAP
GLEKLANILPPRVAAVDTIEKKWAFPDPSRAKEFLFISGTKMRTYARTGENPPDGFMCP
SGWNVLVKYYESLQESEAKQQAVSA"

complement (8394. . 9339)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NVKNYANALKIAMQFPDIQKSGKLENNEISWRCDSGLKDGSEASIDLSKGLYDAGDHM
KFGFPMAFTATVLSWSILEYGDQMASLNLLDHAKDSLKWTTDFLINAHPSPNVLYIQV
GDPVTDHKCWDRPETWTRKRTLIKIDTKTPGTEVAAETAAAMAAASLVFKESDTKYSS
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/db_xref="G1:10086483"
/translation="WHMQLLHNDRVVMYDRTNFGPSNISLPNGNCRDNPQDAVSKIDC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /proteIn id="AAG12562.1"
/db xref="GI:10086502"
/translation="MVAKPRSRCCCCSVFIGVIILIAIIIAVIFTIRHRSNHSDDDGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CGLIPSSPTATSSRTDGGLIWVSEWNALQHPVSSAFLATLYSDYMLTSGYKELSCSDQ
SFKDSDLRKFARSQADYMLGKNPEKMSYLVGYGEKYPEFVHHRGASIPADATTGCKDG
FKWLNSDEPNPNVAYGALVGGPFLNDTFIDARNNSMQNEPSTYNSALVVGLLSSLVTT
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vykrnlimosvskmivkseliddoggelvelivpetelcvkkaesetmpkvklnoldl
ewvhvisegwasplkgfmredeyloslhpnslrlkngffvnmslpivlaidddykeqi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TLLKHAKQLFDFADNNRGSYSVNIPEVQSYYNSTGYGDELLWAASWLYHATEDQTYLD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FVSENGEEFGNFGSPSWFSWDNKLPGTHILLSRLTFFKKGLSGSKGLQGFKETAEAVM
                                                                                                                                                                                       On May 16, 2000 this sequence version replaced gi:7547094.

Bases 60,267-119,942 of BAC clone F6F9 overlap with bases 1-59,676 of IGF clone F14H1, AC024609 and bases 1-3,490 of BAC clone F6F9 overlap with bases 89,221-92,710 of BAC clone T20H2, AC022472.

Location/Qualifiers
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                                             Submitted (12-SEP-2000) DNA Sequencing and Technology Center, Stanford University, 855 California Avenue, Palo Alto, CA 94304,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2448. .4393
/gene="R6F9.1"
join(2448. .2640,2712. .2995,3068. .3502,3589. .3727,
8088. .3974,4064. .4393)
/gene="F6F9.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            complement (join (8394. .8526, 8930. .9215, 9321. .9399))
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gene="F6F9.2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              'note="Similar to endo-beta-1,4-glucanase"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                product="sulfate adenylyltransferase"
protein id="AAG12541.1"
'db_xref="G1:10086481"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    organism="Arabidopsis thaliana"
|mol_type="genomic DNA"
|db_xref="taxon:3702"
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14164. .15678
/gene="F6F9.4"
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/gene="F6F9.2"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                1. .119942
Direct Submission
Submitted (12-SEP
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join(18898. 19093,19182. 19243,19336. 19403,19510. 19631, 19701. 19824,19937. 19988,20276. 20393,20887. 21016, 21098. 21220,21301. 21354,21480. 21661,21734. 22068) join(24177. 24269,24579. 25172,25331. 25510,25592. 25651, 25566. 27256) /gene="F6F9.8" oin(28911. .28985,29480. .29677,29976. .30100,30198. .31062) gene="F6F9.9" QCDWVEMNNGLKKRRWYASNHILPDGKQIVMGGQGQFNYBFFPKTTNPNVVALPFLAE THDQGQENNLYPFVFWNTDGNLFMFANNRAILLDYVKNTVVKTFPAIPGGDPRNYPST GSAVILPLKNLEADNVETEVLVCGGAPKGSYNLARKKTFVKALDTCARIKINDAKPEW HCLLCLQLEVYDGKGSLEAESVEEVKEETLAPKQQAVTKRGASKKRKASKASSDSEQD SDEDNSDKEKEVQGSDADSDYSEDGEEANGKKQSARGRGRGRGRGRGRGSRTSNGKAPP /codon_start=1 |protein_id="MaG12545.1" |db_xref="G1:10086485" |/translation="MQENAPRTMSDVQRVLAISNKVFDMVRLFISEDSPSQVGSESQD complement (join (16924. .17094,17228. .17318,17417. .17496, 17611. .17682))
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COMMENT

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5991B. 61713
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     complement(join(62425. .63429,63528. .63559,63863. .64074,.
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GDVRINTEMPI EPTSDVAVIGNAV VSRONDLS FHGGGLSLSLEGGOIO 105A VSO SPECYTH
GDVRINTEMPI EPTSDVAVIGNAV VSRONDLS FHGGGLSLSLEGGOIO 105A VSO SPECYTH
GONLS NOLLS YNNLAP STRODENGKSLS VHQHHSDOILLPS SVYNNIGNGYGE YNNYR YE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  'note="Similar to homeodomain proteins"
                                                                                                                                                                                                                                                                                                             ر102231. .52584,52917. .53501)
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** المحدد التاليخة ا
                                                                                                                                                                                                                                                                                                                                                                                                                                               note="Hypothetical protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        note="hypothetical protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    complement (54491. .56307)
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                                                                                                                                                                                                                                                 Day 9, 2000 this sequence version replaced gi:7143418.

Bases 1-32,040 of IGF clone F1B16 overlap with bases 97,508-129,547 of IGF clone F10A5, gpl_AC006434.

e-mail for correspondence arab@sequence.stanford.edu Genes with similarity to proteins in the databases are named 'putative', '-like' or 'similar to'. Genes that have EST similarity but no significant protein similarity are described as 'unknown proteins'. Genes that are annotated based only on gene prediction software are described as 'hypothetical proteins'. The gene prediction programs used to predict genes include: Grail (Informatics Group, Oak Ridge National Laboratory, http://compbio.ornl.gov/section/index.html), GENSCAN (Chris Burge, http://genes.mit.edu/GENSCAN), FEXA (Victor Solovyev, Http://genemic.sanger.ac.uk/gf/gf.shtml), and NetPlantGene (S.M. Hebsgaard, et al., CBS, Technical University of Denmark, http://www.cbs.dtu.dk/NetPlantGene.html).
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Altafi,H., Nguyen,M., Lam,B., Southwick,A., Ecker,J., Theologis,A.
and Davis,R.W.
                                                                                                                             Submitted (13-SEP-2000) DNA Sequencing and Technology Center, Stanford University, 855 California Avenue, Palo Alto, CA 94304,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="overlap with bases 97,508-129,547 of IGF clone F10A5, gb|AC006434. See GenBank record for BAC clone F10A5 for annotation in this region." complement (32986. .33822)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /product="Putative ubiquitin-conjugating enzyme"
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                                                                                               Query Match 14.9%; Score 253.4; DB 15; Length 100685; Best Local Similarity 65.4%; Pred. No. 2.6e-40; Matches 371; Conservative 0; Mismatches 196; Indels 0; C
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1064 GGTGAAGAACACGATTCATGACCGTGTCCATTTTGTGAACAAGACATTGGCAGTGGCCCC 1123

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non-coding transcript
probably inactive due to 5'exon missing in CDS"
join(21650. .21946,23314. .23748,25555. .25589,25715. .26667,
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SRGHSLPTDADSWRKARRSPGYQLYRQVSDSKIPSLASINBGASPEGRPSSSMLSVVS
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                           The orientation of the sequence is from SP6 to T7 of the PAC clone. This sequence of P0469E09 clone has an overlap with P0699D11 (DDBJ: AP002817) clone at 5' end and with P0453A06 (DDBJ: AP001383) clone at 3' end. Detailed information on overlap and assembly quality together with annotation of this entry is available at ttogether with annotation of this entry is available at ttogether define at together (Coation) (Qualifiers)
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contains full-length cDNA(s): AK071445"
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/chromosome="1"
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/gene="P0469E09.3"
/note="supported by full-length cDNA(s): AK062597"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="supported by full-length cDNA(s): AK102361"

join(23418. 23748,2555. 25589,25715. 26644)

jone="10469800.4"

hote="contains full-length cDNA(s): AK102361"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .mote="supported by full-length cDNA(s): AK071445" | join(5902. .5980,6229. .6272,8134. .8295) | gene="P0469E09.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="probably inactive due to 3'exon missing probably inactive due to 5'exon missing in CDS pseudogene, Mutator-related transposase"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     complement(21541. .21955)
/gene="P0469E09.3"
/note="contains full-length cDNA(s): AK062597
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miscellaneous feature of the sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .21955)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        complement (21541. . /gene="P0469E09.3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /gene="P0469E09.2"
11101. .12441
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/gene="P0469E09.4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       'gene="P0469E09.2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      clone="P0469E09"
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Direct Submission

Sibmitted (09-Mar.2000) Takuji Sasaki, National Institute of
Direct Submission

Sibmitted (10-Mar.2000) Takuji Sasaki, National Institute of
Agrobiological Sciences, Rice Genome Research Program; Kannondai
2-1-2, Tsukuba, Ibaraki, 305-8602, Japan

(E-mail:tsasaki@nias.affrc.go.jp, URL:http://rgp.dna.affrc.go.jp/,
Tel:81-298-38-7441, Fax:81-298-38-7468)

Genes were predicted from the integrated results of the following:
(E-mail:tsasaki@nias.affrc.go.jp/Robark.hmm], FGENESH
(http://opal.biology_gatech.edu/GeneMark/), GlimmerM
(http://www.tigr.org/tdb/glimmerm/glmr.form.html), RiceHMM
(http://www.tigr.org/tdb/glimmerm/glmr.form.html), splicePredictor
(http://piolinformatics.iastate.edu/GeneMark/), SplicePredictor
(http://plobin.cse.psu.edu/html/docs/sim4.html), gap2
(http://globin.cse.psu.edu/html/docs/sim4.html), gap2
(http://globin.cse.psu.edu/html/docs/sim4.html), gap2
(http://globin.cse.psu.edu/html/docs/sim4.html), gap2
(http://globin.cse.psu.edu/html/docs/sim4.html), gap2
(http://nobi.nlm.nih.gov/blast/db) and the cDNA
sequence was searched against NCBI NonRedundant Protein database
with BLASTP. ESTS represent the identified cDNA sequences using
BLASTN with the corresponding DDBJ accession no.
A gene with identity or significant homologies of the coding
classified based on the protein name to indicate the homology level
such as same name, 'putative' and 'like protein', A gene without
significant homology to any protein be und 'like protein', a gene without
significant homology to any protein with fell beartial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sasaki, T., Matsumoto, T., Yamamoto, K., Sakata, K., Baba, T.,
Katayose, Y., Wu, J., Nimura, Y., Cheng, Z., Nagamura, Y.,
Antonio, B.A., Kanamori, H., Hosokawa, S., Masukawa, M., Arikawa, K.,
Chiden, Y., Hayashi, M., Okancto, M., Ando, T., Aoki, H., Arita, K.,
Hamada, M., Harada, C., Hijishita, S., Honda, M., Ichikawa, Y.,
Idonuma, A., Ilijima, M., Ikeda, M., Ikeno, M., Ito, S., Ito, T., Ito, T.,
Ito, Y., Iwabuchi, A., Kamiya, K., Karasawa, W., Katagiri, S.,
Kikuta, A., Kobayashi, T., Mukai, Y., Nagasaki, M., Makashima, M.,
Nizuno, H., Mizubayashi, T., Mukai, Y., Nagasaki, M., Shimokawa, T.,
Ohta, I., Ono, N., Saji, S., Sakai, K., Shibata, M., Shimokawa, T.,
Shomura, A., Song, J., Takazaki, Y., Terasawa, K., Tsuji, K., Waki, K.,
Yamo, M., Jiang, J., and Gojobori, T., Ito, H., Hahn, J.H., Kim, H.I., Eun, M.Y.,
Yano, M., Jiang, J. and Gojobori, T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BST homology (covering almost the entire length of partial sequence) is classified as an 'unknown' protein. A gene predicted by two or more gene prediction programs is classified as a 'hypothetical' protein according to IRGSP standard. A gene predicted by a single gene prediction program is also classified as a probable 'hypothetical' protein and is included as a
                                                                                                                                                                                                                 Oryza sativa (japonica cultivar-group) genomic DNA, chromosome 1, APO01366 BA000010
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The genome sequence and structure of rice chromosome 1
Nature 420 (6913), 312-316 (2002)
                                                                            87404 TTATTTGGCTGCAACTGATGTGCTTGTTCAGAACTCTCAGGTGAGT 87359
                                         TTACTTGGCAGCAATTGATGTGCTTGTTCAGAATTCTCAGGGCCGT 1169
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TITLE
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AUTHORS
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COMMENT

in CDS

123553

1003

1063

123673

123613

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123852 GTTGCTGAAGATAATGTTGCAAGAAGAGTCCTACGGGAGCATATCCGTGAGTTCCTTGGA 123793
                                                                                                     123552 AGTTGTGGGAAGTGACATAAATGCTCAGACCAAGTTTGAGACACAATTACGTGATTTTGC 123493
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            123492 GGTGAAGAATGGGATTCAGGACCGGGTTCACTTTGTAAACAAGACATTAGCAGTGGCTCC 123433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GGTGAAGAACACGATTCATGACCGTGTCCATTTTGTGAACAAGACATTGGCAGTGGCCCC 1123
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Submitted (26-OCT-2004) Shusei Sato, Kazusa DNA Research Institute,
Submitted (26-OCT-2004) Shusei Sato, Kazusa DNA Research Institute,
Department of Plant Gene Research; 2-6-7 Kazusa-kamatari, Kisarazu,
Chiba, 292-0818, Japan (E-mail:saato@kazusa.or.jp,
UKL:http://www.kazusa.or.jp/, Tel:81-438-52-3935(ex.2337),
Rax:81-438-22-3933),
Rax:81-438-22-3933),
Rax:81-438-22-3933),
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Rax:81-438-22-3933,
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Rax:81-438-22-3933,
Rax:81-438-22-393,
Rax:81-438-22-39
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Lotus cormiculatus var. japonicus
Eukaryota, Virtigiplantae; Stregtophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicctyledons;
rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Loteae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AP008071 92376 bp DNA linear HTG 28-DEC-
Lotus corniculatus var. japonicus chromosome 5 clone LjT12P24,
SEQUENCING IN PROGRESS ***, 21 unordered pieces.
                                                                                                                                                                                                                                                                                                                                                                        123672 TIGATGTTAAAATACAGGTGTTTCACGTGGAAAAGGGCAGGACTTATTTCTTCAAGGCTT
                                                                                                                                                                                                                                                               123732 ATCCCTGTTGTTATTCCAACTATATGTATATTGATTATACCAATTCATTTCTCTGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         123432 TTATTTGGCTGCAACTGATGTGCTTGTTCAGAACTCTCAGGTGAGT 123387
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                                                                      GTACGCAGTGAGGATCTCCTGTTTGCAATAATAACA-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AP008071.1 GI:56806379
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                                                                                                                                                                                                                                                                                                                              protein_id="BAA92400.1"
/db_xref="GI:7228440"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DWI PGNGNELDNSDPHPEPYDAPPSVI STEQLNPAAEPVVGVEAAPVTVAEPDGVTTS
AITANI PSPSDDINLDDWLNELFDPFFDPEQSLASADLSPDEGNVESSNVGALAPKVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         QDYSSPNENVVDDTEYLLPEDVYNILHPGTDDFNMLQNPLDQYPIQYATDVWSGIQKE
ELWSPQANAEPSQSNEAADNGIIRRYRSMKTPETSVPQPKGKTQAKMRVGINKMATSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MGKQTIGTKKTLVFHEGRPPTGRRTEWIMHEYYIDERECQACPDMKDAYVLCRITKRN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SESINOTIKFENSGRLVEHOKNOAHDVASTKRSDAGKPSTELSSNRGFLRGIRNAFAG
                               /gene="P0469E09.5"
/note="supported by full-length cDNA(B): AK102808"
complement(join(27953. .28624,29565. .29918,30369. .30646,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  744 AAAATACAGATGCCACAAACTTATGTTGTTCACCTGGGGAATAGTAAAGAACTAATGGAA 803
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                                                                                                                                                                                                                                                                                                                                                                                                                                       DIYKHEPWDLPAKCDVPTQDNKWHFFAARDRKYPNGSRSNRATVAGYWKS
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Pred. No. 1.5e-34;
0; Mismatches 57; Indels 100; G
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probably inactive due to 5'UTR too long in CDS"
probably inactive due to 5'UTR too long in CDS"
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join(35818. .35866,37294. .37550)
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join(35818. .35866,37294. .37550)
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.31200,32145. .32387))
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contig of 5721 b
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contig of 5018 b
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gap of unknown 1
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Direct Submission

L Submitted (26-007-2004) Shusei Sato, Kazusa DNA Research Institute,
Chiba, 292-0818, Japan (B-mail:ssato@kazusa.or.jp,
Chiba, 292-0818, Japan (B-mail:ssato@kazusa.or.jp,
UKL:http://www.kazusa.or.jp/, Tel:81-438-52-3935 (ex.2377),
Fax:81-438-52-3934)

* NOTE: This is a "working draft' sequence. It currently
* Consists of 21 contigs. The true order of the pieces
* anot known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
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HTG; HTGS_PHASE1.
Lotus corniculatus var. japonicus (Lotus japonicus)
Lotus corniculatus var. japonicus
Lotus corniculatus var. japonicus
Eukaryota; Viridiplantae: Stracheophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; cosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Loteae;
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                                                                                                                                                                                                                                                                                                                                           Gaps
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                                                                 /estimated length=unknown 73437. 73536 /estimated length=unknown 78555. 78654 /estimated length=unknown 84099. 84198
59556. .59<u>6</u>55
/estimated length=unknown
67616. .67715
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/organism="Lotus corniculatus var. japonicus"
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/wariety="japonicus"
/warzef="taxon:34305"
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/clone="LjT2P24"
/lote="Type clone:TM1426, synonym:Lotus japonicus"
17695. 17794
/estimated_ingth=unknown
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9 92376: contig of 8178
Location/Qualifiers
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20156. .20255
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21557. .21666
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39730. 39829
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Eukaryota; Viridipantae; Streptophyta; Embryophyta; Tzacheophyta; Eukaryota; Viridipantae; Streptophyta; Eukaryota; Viridipantae; Streptophyta; Eukaryota; Cre eudicotyledons; rosidas; eurosida II; Brassicales; Brassicaceae; Arabidopsis.

1 (bases 1 to 2013)

1 (bases 1 to 2013)

2 Cheuk, R., Chen, H., Kim, C.J., Shinn, P., Bowser, L., Carninci, P., Dale, J. M., Hayashizaki, Y., Heuan, V.W., Ishida, J., Jones, T., Kamiya, A., Karlin-Neumann, G., Kawai, J., Lam, B., Lin, J., Miranda, M., Narusaka, M., Nguyen, M., Oodera, C.S., Palm, C.J., Quach, H.L., Sakurai, T., Satou, M., Seki, M., Southwick, A., Toriumi, M., Wong, C., Wu, H., C., Yamada, K., Yu, G., Yuan, S., Shinozaki, K., Davis, R.W., Arabidopsis ORF clones
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Direct Submission
Submitted (15-MAY-2003) Salk Institute Genomic Analysis Laboratory
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Pred. No. 1.5e-12;
0; Mismatches 48
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78555. 78654
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KGLDVVANENSEALVNITGKDDAGSNRRTDVSLITKDDGVSRRELSSKQKTRKTVRTS
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GTCDRKSDFKRLVWSRRFVLLPHELSWTGAPTISMELASELLSCGATVSAVVLENSRGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LMOELSRRRIKVEDKGELSFKTAMKADLIIAGSAVCTSWIDQYMNHHPAGGSQIAWW
IMENRRBYFDRAKPVLDRVKMLIFLSESQSRQWLTWCEREHIKLRSQPVIVPLSVNDE
LAPVAGIPSSLNYPTLSPEKMRVKRQILRESVRTELGITDSDMLVMSLSSINPTKGQL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EKOELKVILGSVGSKSNKVGYVKEMLSFLSNSGNLSKSVMMTPATTRVASLYSAADVY
VTNSQGVGETFGRVTIEAMAYGLAVVGTDAGGTKEMVQHNMTGLLHSMGRSGNKELAH
NILYILRNPDERLRLGSEGRKMVEKMYMKQHMYKRFVDVLVKCMRP"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                translation="MEEIRLSPLRQTSVKSSLSGRSTPRGTPRVYSGRTPRRGHGGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LLLESIALALSERGQESQRNHKGIIRKEKVSLSSKHRLRGSSRQMKSVSLTLDNGLRR
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(SIGnAL), Plant Biology Laboratory, The Salk Institute for
Biological Studies, 10010 N. Torrey Pines Road, La Jolla, CA 92037,
                                                                                                                                                                                                             The Salk, Stanford, PGEC (SSP) Consortium members constructed and sequenced the pUNI (ORF) clones using the RAFL CONAS: Cheuk, R., Chen, H., Kim, C.J., Shinn, P., Bowser, L., Chan, M.M., Chang, C.M., Dale, J.M., Hsuan, V.W., Jones, T., Karlin-Neumann, G., Lam, B., Lee, J.M., Lin, J., Miranda, M., Nguyen, M., Ondera, C.S., Palm, C.J., Quach, H.L., Southwick, A., Tang, C.C., Toriumi, M., Wong, C., Wu, H.C., Ecker, J.R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Cheuk, R. (SSP/Salk) and Seki, M. (RIKEN GSC) contributed equally to this work. Shinozaki, K. (RIKEN GSC) and Ecker, J.R. (SSP/Salk) contributed equally to this work as PIs.
                                                                                                        collection and clustering of RAFL CDNAs (RAFL CDNA: 'RIKEN Arbidopels Full-Length CDNA'): Seki,M., Narusaka,M., Ishida,J., Satou,M., Kamiya,A., Sakurai,T., Carninci,P., Kawai,J., Hayashizaki,Y. and Shinozaki,K.
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                                                                                    (GSC) members carried out the
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54.5%; Pred. No. 3.8e-08;
tive 0; Mismatches 155; Indels
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/organiam="Arabidopsis thaliana"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        'note="glycosyl transferase"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /protein_id="AAP3777.1"
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                                                                                    RIKEN Genomic Sciences Center
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product="At1g52420"
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Best Local Similarity 54.5'
Matches 186; Conservative
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                                                                                      COMMENT
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A FOWERS SELVYWILLITYLING TO STAND THE PROBLEM TO THE PROBLEM THE 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta, eudicotyledons, core eudicotyledons, rosids, eurosids II, Brassicales, Brassicaceae, Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 (bases 1 to 2603)
Southwick, A., Nguyen, M., Tripp, M., Palm, C.J., Jones, T., Wu, T.,
Garninci, P., Chen, H., Cheuk, R., Chan, M. M., Chang, C.H., Dale, J.M.,
Deng, J.M., Hayashizaki, Y., Hsuan, V.W., Lee, J.M., Ishida, J.,
Kamiya, A., Kawai, J., Kim, C.J., Narusaka, M., Onodera, C.S.,
Quach, H.L., Sakurai, T., Satou, M., Seki, M., Shim, P., Tang, C.C.,
Shinozaki, K., Ecker, J., Theologis, A. and Davis, R.W.
Direct Submission
Submitted (20-DEC-2002) DNA Sequencing and Technology Center,
Stanford University, 855 California Avenue, Palo Alto, CA 94304,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RIKEN Genomic Sciences Center (GSC) members carried out the collection and clustering of RAFL cDMA (RAFL cDMA: 'RIKEN trabidopsis Full-Length cDMA'): Seki,M., Narusaka,M., Ishida,J., Satou,M., Kamiya,A., Sakurai,T., Carninci,P., Kawai,J., Hayashizaki,Y. and Shinozaki,K.
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                                                                                1966 AIGTACAAGCGATTCGTCGATGTTCTGGTCAAATGCATGAG 2006
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/note="This clone is in pBluescript"
1416 ATGGCTGAGAGGATCGCGGCGGTGTTGAAGGATGTCCTGAG
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Arabidopsis thaliana
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/db_xref="taxon:3702"
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Arabidopsis thaliana gene for hypothetical protein, partial cds, ak221889
                      LAFVAGIPSSLNTPTLSPEKORVKRQILKESVRTELGITDSDMLVMŠLSSINPTKGQL
LILESIJALALSERGOESQRNHKGIIRKEKVSLSSKHRLKGSRRQMKSVSLTLDNGLRR
EKQELKVLLGSVGSKSNKVGYVKEMLSPLSNGNLSKSVMTPATTRVASLYSAADVY
VTNSQCSVGETFGRYTI EAMAYGLAVVGTDAGGTKEMVQHNMTGLLHSWGRSGNKELAH
NLLYLLRNPDERLRLGSEGRKMVEKOYMKQHMYKRFVDVLVKCMRP"
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Large-scale analysis of RIKEN Arabidopsis full-length (RAFL) cDNAs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 An Arabidopsis full-length cDNA library was constructed essentially as reported previously (Seki et al. (1998) Plant J. 15:707-720; Seki et al. (2002) Science 296:141-145).
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Imenrrey forakpvldrvkmli plsesosrowltwceeehi klrsopvi vplsvnde
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Makaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicotyledons,
rosids, eurosids II, Brassicales, Brassicaceae, Arabidopsis.
                                                                                                                                                                                                                                                                                                              GTGGCCCCTTACTTGGCAGCAATTGATGTGCTTGTTCAGAAATTCTCAGGGCCGTGGAGAA
                                                                                                                                                                                                                                                                                                                                                                   2005 GIIGCIICAIIAIACICIGCAGCAGAIGICIACGIIACAAACICCCAGGGAGIIGGIGAA
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                                                                                                                                                                                                         Length 2603;
                                                                                                                                                                                                         5.5%; Score 93; DB 15; Length 26
llarity 54.5%; Pred. No. 3.8e-08;
Conservative 0; Mismatches 155; Indels
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Arabidopsis thaliana (thale cress)
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Matches 186;
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AFVAGUSSSLATPTLTQETMKEKRQKLRESVRTBFGLTDKOMLVMSLSSINPGKGQLL
LLESVALALEREQTQEQVARRNQSKI IKNIMGIRKEKISLSARHRLAGSSRKWKITSP
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EI VEHNVTGLLHPVGRAGNKVLAQNLLFLENPSTRLQLGSQGREI VEKMYMKQHMYK
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/db_xref="G1:6231120"
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This clone is in a modified pBluescript vector. Please visit our web site (http://rarge.gsc.riken.jp/) for further details.
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53.6%; Pred. No. 1.3e-07;
ive 0; Mismatches 163;
                                                                                                        thaliana"
                                                                                                                                                                                                                                'note="common name: thale cress"
                                                                                                    organism="Arabidopsis"
/mol_type="mRNA"
/db_xref="taxon:3702"
                                                                                                                                                                     /chromosome="3"
/clone="RAFL22-26-A16"
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                                                             Location/Qualifiers
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IDENTITY NUC Gapop 10.0 , Gapext 1.0 Scoring table:

9993994 Total number of hits satisfying chosen parameters:

4996997 seqs, 3332346308 residues

Searched:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

N Geneseq 21:* Database :

geneseqn1980s:* geneseqn1990s:*

geneseqn2003cs: geneseqn2001as:* geneseqn2001bs: geneseqn2002as:* geneseqn2003as:* geneseqn2003bs:* geneseqn2000s:* geneseqn2002bs:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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geneseqn2003ds

SUMMARIES

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Result	0.00	Query	Query Match Length DB	Ë	QI.	Description
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т	1647	96.8	1647	13	ADX09132	Adx09132 Plant ful
7	589.6	34.6	1715	m	AAC42068	Aac42068 Arabidops
e	426.2	25.0	1094	13	ADR65394	Adr65394 Cotton cD
4	262	15.4	276	7	ADS71019	Ads71019 Corn seed
S	257	15.1	257	7	ADS71062	Ads71062 Corn seed
9	244.8	14.4	948	13	ADR62845	Adr62845 Cotton cD
0	233	13.7	583	10	ABX56781	Abx56781 Arabidops
60	227	13.3	625	13	ADR62846	Adr62846 Cotton cD
Q	227	13.3	625	13	ACN58791	Acn58791 Cotton gy
10	210	12.3	382	13	ADR65395	Adr65395 Cotton cD
c 11	158.6	9.3	514	13	ACN58833	Acn58833 Cotton gy
12	154.6	9.1	284	٣	AAA31140	Aaa31140 Plant mic
13	74	4.3	1964	13	ADT18408	Adt18408 Plant cDN
14	67.4	4.0	254	σ	ADA60128	Ada60128 Soybean s
15	67.4	4.0	254	12	ADQ06025	Adq06025 Soybean t
16	52.4	3.1	2987	œ	ABT17892	Abt17892 Aspergill
17	52.4	3.1	3495	œ	ABT19706	Abt19706 Aspergill
18	50.4	3.0	90597	10	ADJ72363	Adj72363 Streptomy
19	50.4	3.0	90600	9	ABQ78872	Abq78872 S. roseos

Add29793 Human tum Aaz93717 HSV-1 V22 Adg33861 Kateadcom Abb78691 Kitasatcos Ach12658 Enediyne Acc10251 Kitasatcos Adx49110 Plant ful Aaz30007 Optimised Abs32912 Organopho Ads15486 HSV-1 pol Adx19784 Herpes pol Adx19784 Herpes pol Adx29395 HSV-1 teg Adx29395 HSV-1 VP2 Adx868795 Epitope 1 Add10477 Herpes si Add10477 Herpes si Add10477 Herpes si Ads15488 HSV-1 pol Adx26227 HIV-1 VP2 Adx86468 HSV-1 pol Adx26227 HIV-1 VP2 Adx86468 HSV-1 pol Adx26227 HIV-1 VP2 Adx86468 HSV-1 VP2	6 Phosp 2 Trans Herpes
10 ADD29793 3 AAZ93717 6 ABS78681 14 AER12658 13 AAZ30007 2 AAZ30007 2 AAZ30007 2 AAZ30007 13 ADS15486 2 AAZ307807 12 AAZ9395 6 ABY73163 112 ADG10477 113 ADG10477 114 AAFS6996 6 ABA33386	10 ADF70996 12 ADM83002 2 AAV17085
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0 222222222222222222222222222222222222	1 4 4 4 1 6 4 3

ALIGNMENTS

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plant protectant; plant growth regulant; gene therapy; plant; recombinant DNA construct; physical array; plant breeding marker; cold tolerance; heat tolerance; drought tolerance; herbicide tolerance; streme osmotic condition; pathogen tolerance; pest tolerance; growth rate; cell cycle pathway; disease resistance; galactomannan production; lignin production; plant growth regulator; yield; plant growth; plant development; seed oil; protein yield;
                                                                                     Plant full length insert polynucleotide seqid 3707.
                    ADX09132 standard; cDNA; 1647 BP.
                                                               (first entry)
                                                                                                                                                                                         protein content; gene; ss
                                                                21-APR-2005
                                          ADX09132;
RESULT 1
           ADX09132
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Unidentified.

US2004034888-A1.

19-FEB-2004.

28-APR-2003; 2003US-00425114.

06-MAY-1999; 99US-00304517. LIU J. ZHOU Y. (LIUJ/) (ZHOU/) (KOVA/) (SCRE/)

Tabaska JE, Screen SE, Zhou Y, Kovalic DK, KOVALIC D K. SCREEN S E. TABASKA J E. CAO Y. (TABA/) (CAOY/) Liu J,

Cao Y;

WPI; 2004-180133/17.

New recombinant DNA construct, useful for improving plant tolerance to

us-09-938-294-2.rng

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cold, heat, drought, herbicides, extreme osmotic conditions, pathogens or pests, for conferring increased resistance to plant disease, or for improving yield.
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Claim 1; SEQ ID NO 3707; 15pp; English.

The invention describes a recombinant DNA construct comprising a polynucleotide consisting of a sequence encoding an amino acid sequence available in meletronic form from the US patent office at available in electronic form from the US patent office at the sequence uspto. 2004014888. The polynucleotide of the invention are also useful in physical arrays of molecules and as plant breeding markers. The recombinant DNA construct is useful for improving plant tolerance to cold, heat, drought, herbicides, extreme osmotic conditions, pathogens or pests, for manipulating growth rate in plant cells by modification of the cell cycle pathway, for conferring increased resistance to plant disease, for producing galactomannan, ingnin or plant growth regulators, for increasing the rate of homologous recombination in plants, for improving yield by modification of photosynthesis or carbohydrate, nitrogen or phosphorus use and/or upcake or by providing improved plant growth and development under at least one stress condition or for modifying seed oil or protein yield and/or content. This sequence represents a plant full length insert of the invention

Sequence 1647 BP; 400 A; 384 C; 440 G; 423 T; 0 U; 0 Other;

ö 535 480 540 655 600 715 180 295 240 355 300 415 360 475 420 595 56 ACCGGCGATGGCAAAGACCCCGTCGTTCGCGGTGGCGGCGGTCGCCGGAGGCCGCGCGCC 115 120 235 116 GGTTCACAACCGGACCCAGCTCCTCCTCCTCCTCGTGGCCGTCGCAGCCTCCGCATC 175 9 CACAGCAGGGTTCCTCCTCCGCGGGGGCCTGCGAGACCCTTGCGACGGCCGTGGGGACCC AGCATTTCTTCTGAGGCATGTTGGCTCGCAAGTGGTGGATAACAAACCAGAGATCACA TTTACCAGCTAGAGGACAGGAGGCAGTTGATATTGCTCTAAAAAGCTGATCTGGTTATCTT CCTTCCGAAGATTTTGTGGTGGATCCATGAAATGCGTGGGCATTACTTTAAGGTTGAATA CCTTCCGAAGATTTGTGGTGGTCCATGAAATGCGTGGGCATTACTTTAAGGTTGAATA 1 ACCGGCGATGGCAAAGACCCCGTCGTTCGCGGTGGCGGCGGCGGTCGCCGGGGCCC CGTGCTCCTCGTCTCCCATGAGCTCTCTCTCTCGGTGGTCCACTTTTACTGATGGAATT AAACACTGCTGTTGCTGGCAAGTGGCTTGACCCTGTTCTGAAAGATCATGTTCCTAAAGT GGTTCACAACCGGACCCCGCTCCTCCTCCTCCTCGTGGCCGTCGCAGCCTCCCCCCATC CACAGCAGGGTTCCTCCTCCGCGGTGCCTGCGAGACCCTTGCGACGCCGTGGGGACCC AGAAACAAATGATGTCACATATAGCTTGGAGCATAGGATGTTGAACCATGGAGTGCAGGT TTTACCAGCTAGAGGACAGGAGGCAGTTGATATTGCTCTAAAAGCTGATCTGGTTATCTT CGCCGCCCTCAACACCGCCGTCGCCAGCGGGAGTCCCCTCGGGTTCATGAGGTCCAAGCT CGCCGCCCTCAACACCGCCGTCGCCAGCGGGAGTCCCTCGGGTTCATGAGGTCCAAGCT CGTGCTCCTCGTCCCCATGAGCTCTCCCTCTGGTGGTCCACTTTTACTGAATT AGCATTTCTTCTGAGGCATGTTGGCTCGCAAGTGGTGTGGATAACAAACCAGAGATCACA AGAAACAAATGATGTCACATATAGCTTGGAGCATAGGATGTTGAACCATGGAGTGCAGGT Gaps ö Length 1647; Indels Query Match 96.8%; Score 1647; DB 13; Best Local Similarity 100.0%; Pred. No. 0; Matches 1647; Conservative 0; Mismatches 0; 176 121 241 301 361 536 969 19 236 181 296 356 416 476 421 481 959 a 유 g g 셤 g g ð δ ò 셤 ð 셤 à à ò ò ઠે ద

RESULT 2 AAC42068

qq	601	TGTCAAACATCTTCCCTTTGTTGCTGGAGCCATGATTGAT	0
ò	716	TTGGAATAGCAGGACTAGCGATCGCCTGAAAATACAGATGCCACAAACTTATGTTGTTCA 775	īο
qq	661	TIGGAATAGCAGGACTAGCGATCGCCTGAAATACAGATGCCACAAACTTAIGTTGTTCA 720	0
ò	776	m	Ŋ
Dp	721	cciggggaatagtaaagaactaatggaagtigctgaagacaatgtcgcaagaagagtcct 780	2
δ	836	ACGGGAACATATTCGTGAATCCCTTGGAGTACGAGTGAGGATCTCCTGTTTGCAATAAT 895	ñ
qq	781	acessaratatrostsaatcccrussastacesastsassattectetrostataat 840	0
δλ	968	AAACAGIGIAICACGAGGAAAAGGACATAITICIICAAGCAITITAICAGGCIII 955	ξ.
qa	841	AAACAGIGIAICACGAGGAAAAGGGACAAGACIIAITICIICAAGCAITIIAICAGGCIIT 900	0
δ	926	GCAGCTCATCCAACACGAGAAACTTAAAGTGCCTAGAATACATGCTGTAGTTGTGGGGAAG 101	15
Db	901	GCAGCTCATCCAACACGAGAAACTTAAAGTGCCTAGAATACATGCTGTAGTTGTGGGAAG 960	0
ò	1016	TGATGTTAATGCTCAGACCAAATTTGAGACTCAGTTACGTGACTTTGTGGTGAAGAACAC 107	75
ДQ	961	rgargitaargcicagaccaaarrrgagacrcagtracgrgactrrgrgggggaagaacac 102	20
δ	1076	GATICAIGACCGIGICCAIITIGIGAACAAGACATIGGCAGIGGCCCCTIACITAGGCAGC 113	35
οp	1021	GATICATGACCGTGTCCATITIGTGAACAAGACATTGGCAGTGGCCCCTTACTTGGCAGC 108	80
ò	1136	AATTGATGTGCTTGTTCAGAATTCTCAGGGCCGTGGAGAATGCTTTGGAAGGATAACAAT 119	9
QQ	1081	AATTGATGTTGTTCAGAATTCTCAGGGCCGTGGAGATGCTTTGGAAGGATAACAAT 114	4.
δ	1196	TGAAGCAATGGCATTCAAGTTGCCAGTATTGGGCACGGCTGCTGGAGGGACCACGGAGAT 125	55
QQ	1141	rgaagcaargecarrcaagrrecagrarregecacegecrecregaggaccacegeagar 120	00
δ	1256	CGTCCTGGACGGCTCGACTGGCCTTCTGCATCCTGGGAAGGAGGAGGGCGTGGCGCCTCT 131	55
Ωp	1201	CGTCCTGGACGGCTTCGACTTCTGCATCCTGCTGGGAAGGAGGGCGTGGCGCCTCT 126	9
ò	1316	TGCAAAGAACATCGTCAGACTCGCAAGCCACGCCGAGCAGAGGGTCTCCATGGGGGAAAA 137	7.5
Op Q	1261	TGCAAAGAACATCGTCAGACTCGCAAGCCACGCCGAGCAGAGGGTCTCCATGGGGGAAAA 132	22
δy	1376	376 GGGCTATGGCAGGGTGAAGGAAATGTTCATGGAGCACCACATGGCTGAGAGGATCGCGGC 1431	135
οp	1321	GGGCTATGGCAGGGTGAAGGAAATGTTCATGGAGCACCACATGGCTGAGAGGATCGCGGC 138	8
ò	1436	GGTGTTGAAGGATGTCCTGAGGAAATCACAGAGAGCACTCCAGGTCTTGAGCTTTGCCCTG 149	61
Ob	1381	GGTGTTGAAGGATGTCCTGAGGAAATCACAGGAGCACTCCAGGTCTTGAGCTTTGCCGTG 144	4
ò	1496	CCCATCAGCTTGCGCTAACATGTTGAACTAGATTTTACGGGCTACGCCTACGTGGTTCAG 155	55
οp	1441	CCCATCAGCTTGCGCTAACATGTTGAACTAGATTTTACGGGCTACGCCTACGTGGTTCAG 150	ĕ
à	1556	GCIGTAAACIGTAGATIGCACICIGIIGGICIACITITICACAIICAIGITITACCIAIT 161	515
Ор	1501	GCTGTAAACTGTAGATTGCACTCTGTTGGTCTACTTTTTCACATTCATGTTTTACCTATT 156	99
δ	1616	AGGCCATGTCCCATTCTATTCCAATTCATATAGGTTCTATTTCAATCCATATAGATTAAG 167	575
ΟÞ	1561	AGGCCATGTCCGATTCTATTCCAATTCATAGGTTCTATTTCAATCCATATAGATTAAG 162	22
ò	1676	AGGGATTGAGGAGATTTCAATCTTAGT 1702	
QO	1621	AGGGAITGAGGAGAITTCAAICTTAGI 1647	

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99US-0139463P.
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99US-0139817P.
                                                99US-0140353P.
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       18-JUN-1999;
18-JUN-1999;
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Hybridisation assay; genetic mapping; gene expression control; protein identification; signal transduction pathway; metabolic pathway; promoter; termination sequence; ss.
                                          Arabidopsis thaliana DNA fragment SEQ ID NO: 34167.
AAC42068 standard; DNA; 1715 BP
                                                                                                                                           9905-0121825P

9905-0123180P

9905-0125784P

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99US-0139119P.
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                           (first entry)
                                                                                    Arabidopsis thaliana
                                                                                                  EP1033405-A2
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             AAC42068;
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531 506 591	OY SECTORISTIC TO A A A A A A A A A A A A A A A A A A		806 TGCTGAAGACAATGCGCAAGAAGACCCTACGGGAACATATTCGTGAATCCCTTGGAGT		1046 1131 1106 1191	Oy 1166 CCGTGGAGAATGCTTTGGAAGGATAACAATTGAAGCAATGGCATTCAAGTTGCCAGTATT 1225 Db 1251 CAGAGGAGAATGCTTTGGGAAATAACAATCGAAGGCCTTTAAGCTACCTGTACT 1310 Oy 1226 GGGCACGGCTGCTGCAGGAACCACGGAAGATCGTCCTGGACTGGCCTTCTGCA 1285 Db 1311 TGGTACTGCAGGAGCACAATGGAGAATTGTAGTGAATGGAAAGGACTGGTTACTACA 1370	1311 TAGTGCAGGAAAGAGGGGGAAAGAGCTTCGCCAAGAACATAGTGAAGTTGGCGCA 1346 CGCCGAGCAAGAAGAGGAGTGATACCTCTCGCCAAGAACATAGTGAAGTTGGCGACGCA 1346 CGCCGAGCAGAAGAGGGGAAAAAGGGCTATGGCAGGAAATGTTCAT 1431 AGTTGAGTTACGGCTGAGAAAAAATGGCTATGAGGAAATGTTTTT 1406 GGAGCACCACATGGCTGAGAAAAAAATGGCTTTGAAGGATGTTTTTTTT
AUG-1999; AUG-1999; AUG-1999; AUG-1999; AUG-1999; AUG-1999;	AUG-1999; AUG-1999; SEP-1999; SEP-1999; SEP-1999;	SEP-1999; SEP-1999; SEP-1999; SEP-1999; SEP-1999; SEP-1999;		000000000000000000000000000000000000000	21-OCT-1999; 99US-0160768P. 21-OCT-1999; 99US-0160770P. 21-OCT-1999; 99US-0160815P. 22-OCT-1999; 99US-0160810P. 22-OCT-1999; 99US-0160980P. 22-OCT-1999; 99US-0160980P. 22-OCT-1999; 99US-0160980P. 25-OCT-1999; 99US-016140	000000000000000000000000000000000000000	Query Match 34.6%; Score 589.6; DB 3; Length 1715; Best Local Similarity 68.1%; Pred. No. 5e-156; Indels 0; Gaps 0; 26 GAGTCCCTCGGGTTCATGAGGTCCAAGTCGTCCCCATGAGCTCTCCCT 325 IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII

2;

.9e-110;

Pred. No.

65.0%;

Best Local Similarity

739 132 799 192

72

B

ADR65394 standard; cDNA; 1094

New recombinant nucleic acid molecules and polypeptides from Gossypium hirsutum, useful for producing plants with improved biological characteristics (e.g. improved plant cold or drought tolerance). Cotton; 88; plant; cold tolerance; growth rate; cell cycle pathway; drought tolerance; plant disease resistance; galactomannan; lignin; plant growth regulator; heat tolerance; herbicide tolerance; homologous recombination; extreme osmotic condition tolerance; pathogen resistance; pest resistance; yield; photosynthesis; seed oil; BP; 335 A; 209 C; 258 G; 292 T; 0 U; 0 Other; sequence, SEQ ID 6175 29-JAN-2004; 2004US-00767795 07-MAY-2001; 2001US-00849529 12-DEC-2001; 2001US-00021323 Cao Y; entry) did not form part Zhou Y, (first WPI; 2004-667718/65. Gossypium hirsutum KOVALIC D resistance US2004181830-A1 Sequence 1094 CAO Y DK, 02-DEC-2004 Cotton cDNA 16-SEP-2004 (KOVA/) (ZHOU/) (CAOY/) Kovalic stress

The invention relates to a recombinant polymucleotide comprising any of the 58798 Cotton plant cDNA sequences mentioned in the specification.

CC the 58798 Cotton plant cDNA sequences mentioned in the specification.

CC ansor a recombinant polypeptide comprising any producing a plant having an improved property.

CC comprises transforming a plant with a recombinant construct comprising a promoter region functional in a plant cell operably joined to a promoter region functional in a plant cell operably joined to a polypeptide associated by with the property, and growing the transformed plant. The polypeptide is useful for improving plant coll tolerance, manipulating growth rate in plant cells by modification of the cell cycle pathway, improving plant country in plant of the cell cycle pathway, improving plant tolerance, producing galactomannan (or Inginio or plant growth regulators), improving plant the atte of homologous recombination in plants, improving plant tolerance to extreme osmocic conditions or to pathogens or pested; improving plant conditions or pathogens or pested; improving plant companied by modification of photosynthesis, modifying seed oil or protein yield and/or content, improving yield by modification of carbohydrate, nitrogen or phosphorus use and/or uptashe, or improving yield by providing improved plant growth and development under at least one stress condition. The polymucleotide and polypeptide may also be used in recombinant DNA content can in commuter hased storage and analysis and systems the present companies. of the printed specification, but was obtained the invention. NOTE: The sequence data polynucleotide sequences were available, the remaining 52213 polynucleotides and all 58798 protein sequences were not present or in computer-based storage and analysis systems. The present is a Cotton plant cDNA of the invention. NOTE: The sequence day seqdata.uspto.gov/sequence.html?DocID=20040181830. However electronic format directly from USPTO at SEQ ID NO 6175; 14pp; English

DB 13; Length 1094;

25.0%; Score 426.2;

Query Match

CICIGIIGGICIACIIIIICACAIICACAIGIIIIACCIAIIAGGCCAIGICCGAIICIAII 1635 TGAGACTCAGTTACGTGACTTTGTGGTGAAGAACACGATTCATGACCGTGTCCATTTTGT 1099 TAAAGTGCCTAGAATACATGCTGTAGTTGTGGGAAGTGATGTTAATGCTCAGACCAAATT 1039 TGTTGAACTAGATTTTACGGGCTACGCCTACGTTCAGGCTGTAAACTGTAGATTGCA 1575 313 GCAGGATCTCTTCTACGCGCTTTCTACGAGGCCTTACAACTGATCAAGCAAAAGAAAT 372 GGAAATCACAGGAGCACTCCAGGTCTTGAGCTTTGCCGTGCCCATCAGCTTGCGCTAACA <u> AATTACAATGAGGTATATCCAGTTTTCAATCAATATAATGGAGTGACATCTTTAATTCTG</u> GCCGAAGATTAAAATGCCTGAGACCTATGTTGTTCACCTTGGAAATAGCAATGAACTGAT ecaagriigeagaagacagrigigecraaaagggiirriigegrgaacargriigigaareger TGGAGTACGGAGTGAGGATCTCCTGTTTGCAATAATAAACAGTGTATCACGAGGAAAGGG GAACAAGACATTGGCAGTGGCCCCTTACTTGGCAGCAATTGATGTGCTTGTTCAGAATTC TCAGGGCCGTGGAGAATGCTTTGGAAGGATAACAATTGAAGCAATGGCATTCAAGTTGCC AGT----ATTGGGCACGGCTGCTGGAGGGACCACGGAGATCGTCCTGGACGGCTCGACTG rerecreacadedaacaderecedededeacadaaacadaaaradaaacadaaadada GTTTATTGCACCCTGCTGGGAAAGAAGGGGTGACAACTCTGGCGAAACATATTGTGAAAC TCGCAAGCCACGCCGAGCAGAGGGTCTCCATGGGGGAAAAGGGCTATGGCCAGGGTGAAGG <u> aaagartrcragaacarcacarcecagagagaarregrgaagracrraaagaagcerrga</u> -----GGACTAGCGATCG <u>Argarricaricacaccacacacaararrigaagaaracccacececececececece</u> CCTGAAAATACAGATGCCACAAACTTATGTTGTTCACCTGGGGAATAGTAAAGAACTAAT GGAAGTTGCTGAAGACAATGTCGCAAGAAGAGTCCTACGGGAACATATTCGTGAATCCT ACAAGACTTATTTCTTCAAGCATTTTATCAGGCTTTGCAGCTCATCCAACACGAGAAACT 373 gcaggreccarrecarecarecacrarrereceaacrecareacracarecaracer GAACAAAACTCTAACAGTAGCTCCATATTTAGCTGCCGTAGATGTTCTTGTTCAGAATTC GCCTTCTGCATCCTGCTGGGAAGGAGGGCGTGGCGCCTCTTGCAAAGAACATCGTCAGAC <u>TAGCTACGCATGTAGAGAGGAGGCTTACAATAGGAAAGAGGGGTACGAAAGGGGTGAAAG</u> AAATGTTCATGGAGCACCACATGGCTGAGAAGGATCGCGGCGGTGTTGAAGGATGTCCTGA ATGCGTGGGCATTACTTTAAGGTTGAATATGTCAAACATCTTCCCTTTGTTGCTGGAGCC Areceaegeceartretriaaarragagraretraaagecaregaacerererererega 433 itgaaattggaattacgagcriatgiaacacagaagaaaattcaagarcgigircactrifgr Gaps 11; Indels ATGATTGATTCTCATACAACGGCTGAGTATTGGAATAGCA-Mismatches 348; ö 666; Conservative CCAAT 1640 1040 1100 1220 1276 1336 1456 1516 1576 973 1636 740 193 860 253 920 980 553 613 673 733 793 853 913 13 687 133 800 493 1160 1396 73 Matches ଚ 셤 ð 셤 ò 셤 ò 셤 ò g ઠ g ð 셤 à 셤 ð 유 8 셤 Š g ð 셤 ઠે a à g ò g δ 욥, ò 유 sednence

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CAAATTTGAGACTCAGTTACGTGACTTTGTGTGAAGAACACGATTCATGACCGTGTCCA

1033 ACATT 1037

셤

The invention relates to a corn seedling-derived polymucleotide (cdp)
selected from ADS64985-ADS71316, or their complements and fragments. Also
included are a composition for the detection of altered expression of a
cdp (comprising a polymucleotide selected from ADS64985-ADS71316), a
cdp (comprising a polymucleotide in a biological sample using a cdp,
cdp an expression polymucleotide in a biological sample using a cdp, a
ceedling specific regulatory element that regulates the expression of a
seedling specific regulatory element that regulates the expression of a
cdp, an expression vector containing a cdp or regulatory element, a plant
transformed with the vector, a host cell containing the vector (and
expressing a compound which binds a CDP and screening a plurality of
compounds for binding to cdp polymucleotide. The cdp polymucleotides,
compounds for binding to cdp polymucleotide. The cdp polymucleotides,
compounds for binding to and antibodies are useful for the
dentification, evaluation and alteration, fungal disease, bacterial
cdisease resistance (e.g. to insect infestation, fungal disease, bacterial
infection, Goss' Bacterial Wilt, blight, Stewart's bacterial Wilt, Holcus
spot, bacterial leaf blight, leaf spot, bacterial stripe and maize dwarf
mosaic virus infection) and resistance to environmental stress (e.g.
water stress, pH stress, temperature stress, pollution, injury or
pesticides. The present sequence is cdp cDNA sequence. Corn; seedling-derived polynucleotide; cdp; ss; plant; seed growth; seed development; disease resistance; insect infestation; fungal disease; bacterial infection; Goss' Bacterial Wilt; blight; Stewart's bacterial Wilt; Holcus store; bacterial leaf blight; leaf spot; bacterial stripe; maize dwarf mosaic virus infection; environmental stress; water stress; pH stress; temperature stress; New corn seedling-derived polynucleotides and polypeptides, useful in identifying and altering desired characteristics associated with growth and development, disease resistance, environmental adaptability, quality Corn seedling-derived polynucleotide (cpds), SEQ ID 6035. Sequence 276 BP; 64 A; 58 C; 83 G; 69 T; 0 U; 2 Other; Claim 3; SEQ ID NO 6035; 33pp; English BK; ADS71019 standard; cDNA; 276 BP Sherman 06-AUG-2001; 2001US-00923876 98US-0085331P pollution, injury, pesticide 99US-00298329 (first entry) (INCY-) INCYTE PHARM INC Ito LY, WPI; 2002-195165/25 US2003237110-A9. 12-MAY-1998; 21-APR-1999; Lalgudi RV, 18-NOV-2004 25-DEC-2003 yield Zea mays. ADS71019; and

1; Gaps

Ouery Match
Best Local Similarity 99.3%; Pred. No. 1.6e-63;
Matches 273; Conservative 0; Mismatches 1; Indels

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1213
                                                                                                                                                                                                      GTTGCCAGTATTGGGCACGCTGCTGGAGGACCACGGAGATCGTCGTGGACGGCTCGAC 1273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to a corn seedling-derived polynucleotide (cdp) selected from ADS64985-ADS71316, or their complements and fragments. Also included are a composition for the detection of altered expression of a cdp (comprising a polynucleotide selected from ADS64985-ADS71316), a method of detecting a polynucleotide in a biological sample using a cdp, a method for using oligomers (and amplification) to recover a regulatory element from a DNA library using oligomers designed against a cdp, a seedling specific regulatory element that regulates the expression of a cdp, an expression vector containing a cdp or regulatory element, a plant transformed with the vector, a host cell containing the vector (and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Corn; seedling-derived polynucleotide; cdp; ss; plant; seed growth; seed development; disease resistance; insect infestation; fungal disease; bacterial infection; Goss' Bacterial Wilt; blight; Stewart's bacterial Wilt; Holcus spot; bacterial leaf blight; leaf spot; bacterial stripe; malze dwarf mosaic virus infection; environmental stress; water stress; pH stress; temperature stress;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New corn seedling-derived polynucleotides and polypeptides, useful in identifying and altering desired characteristics associated with growth and development, disease resistance, environmental adaptability,.quality
                                                                                 61 TTTTGTGAACAAGACATTGGCAGTGGCCCCTTACTTGGCAGCAATTGATGTGCTTGTTCA
                                                                                                                                                                                                                                  181 GTTGCCAGTATTGGGCACGACGACGACGAGGAGACCACGGAGATCGTCCTGGACGTCGAC
1 CAAATTTGAGACTCAGTTACGTGACTTTGTGGTGAAGAACACGATTCATGACCGTGTCCA
                                                                                                                               GAATTCTCAGGGCCGTGGAATGCTTTGGAAGGATAACAATTGAAGCAATGGCATTCAA
                                                                                                                                                     TTTTGTGAACAAGACATTGGCAGTGGCCCCTTACTTGGCAGCAATTGATGTGCTTGTTCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Corn seedling-derived polynucleotide (cpds), SEQ ID 6078.
                                                                                                                                                                                                                                                                                    1274 TGGCCTTCTGCATCCTGGGAAGGAGGGCGTGG 1308
                                                                                                                                                                                                                                                                                                              241 TGGCC-TCTGCATCCTGCTGGGAAGGAGGCGTGG 274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 3; SEQ ID NO 6078; 33pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sherman BK;
                                                                                                                                                                                                                                                                                                                                                                                                                       ADS71062 standard; cDNA; 257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          pollution; injury; pesticide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               06-AUG-2001; 2001US-00923876.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   98US-0085331P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 18-NOV-2004 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (INCY-) INCYTE PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Lalgudi RV, Ito LY,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2002-195165/25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   12-MAY-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         21-APR-1999;
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                                                     1094
                                                                                                                               1154
                                                                                                                                                                                                          1214
                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADS71062;
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ADS71062
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                                                                                                                                                                                                                                                                                                                           1035 AAATTTGAGACTCAGTTACGTGACTTTGTGGTGAAGAACACGATTCATGACCGTGTCCAT 1094
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AATTCTCAGGGCCGTGGAGAATGCTTTGGAAGGATAACAATTGAAGCAATGGCATTCAAG 1214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1215 TTGCCAGTATTGGGCACGCTGCTGGAGGGACCACGGAGATCGTCCTGGACGGCTCGACT 1274
           identifying a compound which binds a CDP and screening a plurality of compounds for binding to cdp polynucleotide. The cdp polynucleotides, proteins, vectors, cells and antibodies are useful for the identification, evaluation and alteration of seed growth and development, disease resistance (e.g. to insect infestation, fungal disease, bacterial infection, Goss' Bacterial Wilt, blight, Stewart's bacterial Wilt, Holcus mosaic virus infection) and resistance to environmental stress (e.g. water stress, pH stress, temperature stress, pollution, injury or pesticides. The present sequence is cdp cDNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    240
                                                                                                                                                                                                                                                                                                                                                                                                                                     61 TTTGTGAACAAGACATTGGCAGTGGCCCCTTACTTGGCAGCAATTGATGTGCTTGTTCAG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            121 AATTCTCAGGGCCGTGGAATGCTTTGGAAGGATAACAATTGAAGCAATGGCATTCAAG 180
                                                                                                                                                                                                                                                                                                                                                               9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                drought tolerance; plant disease resistance; galactomannan; lignin; plant growth regulator; heat tolerance; plant growth regulator; extreme osmotic condition tolerance; homologous recombination; extreme osmotic condition tolerance; pathogen resistance; pest resistance; yield; photosynthesis; seed oil;
 CDP), an anti-CDP antibody
                                                                                                                                                                                                                                                                                                                                                                                                   1095 TTTGTGAACAAGACATTGGCAGTGGCCCCTTACTTGGCAGCAATTGATGTGCTTGTTCAG
                                                                                                                                                                                                                                                                                                                                                  AAATTTGAGACTCAGTTACGTGACTTTGTGGTGAAGAACACGATTCATGACCGTGTCCAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    181 TTGCCAGTATTGGGCACGGCTGCTGGAGGGACCACGGAGATCGTCCTGGACGCTCGACT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               plant; cold tolerance; growth rate; cell cycle pathway
                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                               Query Match
15.1%; Score 257; DB 7; Length 257;
Best Local Similarity 100.0%; Pred. No. 4e-62;
Matches 257; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                 Sequence 257 BP; 61 A; 55 C; 73 G; 68 T; 0 U; 0 Other;
 corn seedling derived protein,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Cotton cDNA sequence, SEQ ID 3626.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADR62845 standard; cDNA; 948 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GCCTTCTGCATCCTGC 1291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       07-MAY-2001; 2001US-00849529
12-DEC-2001; 2001US-00021323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       29-JAN-2004; 2004US-00767795
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Cao Y;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GGCCTTCTGCATCCTGC
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ZHOU Y.
CAO Y.
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(ZHOU/) Z
(CAOY/) C
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The invention relates to a recombinant polymucleotide comprising any of the 58798 Cotton plant CDNA sequences mentioned in the specification.

Also a recombinant polypeptide comprising any of the 58798 amino acid sequences mentioned in the specification and producing a plant with a recombinant construct comprising an improved property. Producing a plant with a recombinant construct comprising a plant with a recombinant construct comprising a promoter region functional in a plant cell operably joined to a promoter region functional in a plant cell operably joined to a promoterty, and growing the transformed plant. The polymetide is useful for improving plant cold tolerance for a polypeptide associated with the property, and growing the transformed plant. The polypeptide is useful for improving plant cold tolerance, manipulating growth rate in plant cells by modification of the cell cycle pathway, improving plant drought tolerance, providing increased resistance to plant disease, to producing galactomannan (or lignin or plant growth regulators), improving plant heat tolerance, improving plant tolerance to herbicides, increasing the rate of homologous recombination in plants, improving plant tolerance to extreme osmotic conditions or to pathogens or pests, improving yield by modification of photosynthesis, wodifying seed oil or proteath yield and/or content, improving yield by modification of carbohydrate, introgen cor phospinus use and/or uptake, or improving yield by providing improved plant growth and development under at least one stress condition. The polymucleotide and polypeptide may also be used in recombinant DNA content sequence constructs, in physical arrays of molecules, as plant breeding markers, constructs, in physical arrays of molecules.

Constructs, in physical arrays of molecules, as plant breeding markers, constructs, in the present sequence the present sequence is a cotton plant form plant from the printed specification, but was obtained in a larrancy of man consult. 368 512 GTCACATATAGCTTGGAGCATAGGATGTTGAACCATGGAGTGCAGGTTTTACCAGCTAGA 488 608 692 752 Gossypium 249 ACCGCCGTCGCCAGCGGAGTCCCCTCGGGTTCATGAGGTCCAAGCTCGTGCTCCTCGTC 393 ATCGCGCTGTGAAGCCGAGTCCGCTTAAGCTTTATGAAGTCCACGCGTCCGCTGCTGGTT TCCCATGAGCTCTCCCTCTCTGGTGGTCCACTTTTACTGATGGAATTAGCATTTCTTCTG 453 receiecide de la receienta GTAACATATAGTTTTAGAACATAAGATGTTGGACAGAGGAGTACAGGTTATCTCAGCTAAG GCTGGCAAGTGGCTTGACCCTGTTCTGAAAGATCATGTTCCTAAAGTCCTTCCGAAGATT GCTGGGAAATGGCTGGATGTTGTTCTTAAGGAGATGTTCATCGTGTTCTGCCTAAGGTG AGGCATGTTGGCTCGCAAGTGGTGTGGATAACAAACCAGAGATCACAAGAAACAAATGAT GGACAGGAGGCAGTTGATATTGCTCTAAAAGCTGATCTGGTTATCTTAAACACTGCTGTT TIGTGGTGGATCCATGAAATGCGTGGGCATTACTTTAAGGTTGAATATGTCAAACATCTT only 6585 .Gaps polynucleotide sequences were available, the remaining 52213 polynucleotides and all 58798 protein sequences were not present. ä, New recombinant nucleic acid molecules and polypeptides from Go hirsutum, useful for producing plants with improved biological characteristics (e.g. improved plant cold or drought tolerance) Query Match 14.4%; Score 244.8; DB 13; Length 948; Best Local Similarity 68.8%; Pred. No. 2.5e-58; Matches 352; Conservative 0; Mismatches 157; Indels 3; in electronic format directly from USPTO at segdata.uspto.gov/sequence.html?DocID=20040181830. However Sequence 948 BP; 242 A; 195 C; 220 G; 291 T; 0 U; 0 Other; Claim 1; SEQ ID NO 3626; 14pp; English. WPI; 2004-667718/65 309 369 429 573 489 633 549 693 609 ઠ 셤 8 셤 δ g ઠે 셤 ઠે 셤 ò 셤 ₽

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Gossypium hirsutum
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           872
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Novel Arabidopsis thaliana nucleic acid useful for identifying homologous or related genes, and to create genetically modified and transgenic organisms, such as plant cells and plants.
Hamilton CM, Price JL, Raines TM, Yu Y;
1, Mathew AV, Ledford BL, Woessner JP, Haas WD;
M, Slater T, Davis KR, Allen K, Hoffman N;
                                                                                                                                                                        Thale cress, gene; ds, genetic manipulation; plant, biosynthesis; genetic modification; environmental stress; disease resistance;
                            757
                                             AGTACTAAAGAACGTTTGAAGTTTAAAATGTC 904
                            AGGACTAGCGATCGCCTGAAAATACAGATGCC
                                                                                                                                                     Arabidopsis thaliana polynucleotide #133
                                                                                                                                                                                           fungicide; insecticide; stress tolerance
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                                                                                              ABX56781 standard; DNA; 583
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Page A, Ma
Kricker M,
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PRICE J L.
RAINES T M.
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MATHEW A V.
LEDFORD B L.
WOESSNER J P.
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GARCIA C A.
KRICKER M.
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DAVIS K R.
ALLEN K.
HOFFMAN N.
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Garcia CA,
Hurban P;
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environmental stress, for enhancing or inhibiting production of biosynthetic products in plants and to create genetically modified and transgenic organisms, such as plant to cast genetically modified and are useful for introducing or improving disease resistance and stress tolerance in plants, screening biologically active agents, such as fungicides and insecticides, and for elucidating biochemical pathways. Sequences ABX56649-ABX57647 represent Arabidopsis thaliana plantways of the invention. Note: The sequence date for this patent did not form part of the printed specification but was obtained in electronic format directly from USPTO at seqdata.uspto.gov/sequence.html
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   388 GIICIIGICCAAAACICCCAAGCCAGAGAAAIGCIIIGGGAGAAIAACAAICGAAGCC 329
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        508 AGCAAGCAGACAAGTTCGAGACAGAGCTACGCAACTTTGTCCGAGAAAAGAAACTTGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1083 GACCGTGTCCATTTTGTGAACAAGACATTGGCAGTGGCCCCTTACTTGGCAGCAATTGAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 583;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   13.7%; Score 233; DB 10; Length 5 66.3%; Pred. No. 4.2e-55; ive 0; Mismatches 170; Indels
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Best Local Similarity 66.3
Matches 335; Conservative
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CCTAAGGTGTTGTGGTGGATCCATGAAATGCGAGGCCATTACTTCAAATTAGAGTATGTA 618
   379 ACTGATGAAGTAATATATATAGTTTAGAACATAAGATGTTGGACAGAGGAGTGCAGGTTTTC 438
                                                                                                                                                                                                                                499 ACAGCGGTTGCTGGGAAATGGGTAGATTATGTTCTTAAGGAAGATATTCACCGTGTTCTG 558
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Cotton; plant; BST; expressed sequence tag; transgenic plant; gynoecium; varitety Nucotton13B; library LIB3829; molecular tag; molecular marker; genetic mapping; molecular mapping; seed germination; plant growth; plant quality; plant yield; plant breeding; tissue printing; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Cotton gynoecium tissue EST Clone ID: LIB3829-012-Q6-K6-G10, SEQ:13572.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New isolated nucleic acid molecule that encodes a plant protein or its fragment, useful for isolating a variety of agronomically significant genes associated with plant growth, quality or yield, and as molecular
                                                                                                                                                                                                                                                                                            CCGAAGATTTTGTGGTGGATCCATGAAATGCGTGGGCATTACTTTAAGGTTGAATATGTC
                                                            480 CCAGCTAGAGGACAGGAGGCAGTTGATATTGCTCTAAAAGCTGATCTGGTTATCTTAAAC
                                                                                                                   439 TCCGCGTTTGGAAAAGAAGCTATAGATACTGCTCTAAGAGCTGATTTGGTTGTTTTGAAC
                                                                                                                                                                         ACTGCTGTTGCTGGCAAGTGGCTTGACCCTGTTCTGAAAGATCATGTTCCTAAAGTCCTT
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(FENG/) FENG P C C.
(FINC/) FINCHER K L.
(ZIEG/) ZIEGLER T E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Deikman J, Feng PCC,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to a recombinant polymuclectide comprising any of the 58798 Cotton plant cDNA sequences mentioned in the specification.

CC the 58798 Cotton plant cDNA sequences mentioned in the specification.

CC sequences mentioned in the specification and producing a plant having an improved property comprises transforming a plant with a recombinant construct comprising a comprise transformed property of plant with a recombinant construct comprising a promoter region functional in a plant cell operably joined to a promoter region functional in a plant cell operably joined to a promoterty, and growing the transformed plant. The polypeptide is constituted in moroving plant cold tolerance for a polypeptide associated constitution of the cell cycle pathway, improving plant cold tolerance, manipulating growth rate in plant tolerance, providing increased resistance to plant disease, corought tolerance, improving plant tolerance to plant disease, improving plant have tolerance in moroving plant tolerance to herbicides, increasing conditions or plant growth regulators), improving plant tolerance conditions or to pathogens or pests, improving yield by modification of photosynthesis, modifying seed oil or protein yield by modification of and/or uptake, or improving yield by providing improved plant growth and development under at least one stress condition. The constructs, in physical arrays of molecules, as plant breeding markers, or in computer-based storage and analysis systems. The sequence data for this condition to form part of the printed specification, but was obtained in electronic format directly from USPPO at condition, but was obtained in electronic format directly from Sequence and systems. The sequence and condition are asset and sequence are asset and sequence and sequence are asset in computer sove sequence the printed sequence and an electronic format directly from USPPO at the present sequence and sequence are asset as a sequence and sequence and sequence are asset as a sequence and sequence ar
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Pred. No. 2.2e-53;
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                                                                                                                                                                      07-MAY-2001; 2001US-00849529
12-DEC-2001; 2001US-00021323
                                                                                                             29-JAN-2004; 2004US-00767795
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Best Local Similarity 70.7%;
Matches 302; Conservative
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                                                                                                                                                                                                                                                     (KOVA/) KOVALIC D K. (ZHOU/) ZHOU Y. (CAOY/) CAO Y.
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29-JAN-2004; 2004US-00767795. 07-MAY-2001; 2001US-00849529 12-DEC-2001; 2001US-00021323

16-SEP-2004.

Gossypium hirsutum. US2004181830-A1.

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links in metabolic and catabolic pathways. The mucleic acid molecules are also useful for identifying genes important in initiating and maintaining seed germination or that may be used to mitigate stresses encountered during seed germination. The ESTs additionally enable the acquisition of promoters and cis-regulatory elements which will be useful to express agronomically significant genes in these tissues and/or other tissues, and also permits the acquisition of molecular markers useful in breeding schemes, genetic and molecular markers useful in breeding schemes, genetic and molecular mapping, and in cloning of agronomically detecting the expression level or pattern of a protein or mRNA and for detecting the presence or quantity of a protein by tissue printing. The present sequence represents a specifically claimed EST isolated from a cotton variety Nucotton338 gynoecium tissue cDNA library (LIBB229). The sequence data for this patent did not form part of the printed sequence data for this patent did not form part of the printed sequence data for this patent did not form part of the printed sequence data for this patent did not form part of the printed sequence format for the printed sequence format directly from the US
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Pred. No. 2.2e-53;
0; Mismatches 125; Indels
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Best Local Similarity 70.7%;
Matches 302; Conservative
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New recombinant nucleic acid molecules and polypeptides from Gossypium hirsutum, useful for producing plants with improved biological characteristics (e.g. improved plant cold or drought tolerance).

Cao Y;

Kovalic DK, Zhou Y,

WPI; 2004-667718/65.

(KOVA/) KOVALIC D K.

(ZHOU/) ZHOU Y. (CAOY/) CAO Y.

Claim 1; SEQ ID NO 6176; 14pp; English.

The invention relates to a recombinant polymucleotide comprising any of the 58798 Cotton plant CDNA sequences mentioned in the specification.

The Also a recombinant polypeptide comprising any of the 58798 amino acid sequences mentioned in the specification and producing a plant having an improved property.

Comprises transforming a plant with a recombinant construct comprising a promoter region functional in a plant cell operably joined to a promoter region functional in a plant cell operably joined to a promoter region functional in a plant cell operably joined to a promoter, and growing the transformed plant. The polypeptide is useful for improving plant cold tolerance, manipulating growth rate in plant cells by modification of the cell cycle pathway, improving plant cold tolerance, manipulating growth rate in congulators, improving plant tolerance to plant disease, increasing producing galactomannan (or lignin or plant sylend to perance, improving plant tolerance to herbicides, increasing producing plant colling plant tolerance to herbicides, increasing the rate of homologous recombination in plants, improving plant tolerance to extreme osmotic conditions or to pathogens or peets, improving plant tolerance to herbicides, increasing to extreme osmotic conditions or to pathogens or peets, improving yield by modification of carbohydrate, nitrogen or phosphorus use and/or uptake, or improving yield by providing improved plant growth and development under at least one stress condition. The collant growth and development under at least one stress condition. The collant content, improving yield by modification of carbohydrate, nitrogen or in computer-based storage and analysis systems. The present sequence is a Cotton plant cDNA of the printed specification, but was obtained to patent did not format directly from USPFO at the printed specification, but was obtained to patent with the process of the printed specification of long to the present of the printed specification of long to the present of the printed speci ö 989 746 Argarrigarricacacgrcacacagaararriggaagaaraggacrcaagaggegrigaag 132 806 13 Ardcdaddccarrrcrararradagrardraaacarccaccarcraraccraca 72 ATGATTGATTCTCATACAACGGCTGAGTATTGGAATAGCAGGACTAGCGATCGCCTGAAA ATACAGATGCCACAAACTTATGTTGTTCACCTGGGGAATAGTAAAGAACTAATGGAAGTT 627 ATGCGTGGGCATTACTTTAAGGTTGAATATGTCAAACATCTTCCCTTTGTTGCTGGAGCC segdata uspto gov/seguence.html?DocID=20040181830. However only 6585 polynucleotide seguences were available, the remaining 52213 polynucleotides and all 58798 protein seguences were not present. Gaps ö Query Match
Best Local Similarity 73.8%; Pred. No. 1.1e-48;
Matches 267; Conservative 0; Mismatches 95; Indels Sequence 382 BP; 112 A; 76 C; 94 G; 100 T; 0 U; 0 Other; 687 73 747 셤 셤 ð ò ò

Cotton, ss; plant, cold tolerance; growth rate, cell cycle pathway; drought tolerance; plant disease resistance; galactomannan; lignin; plant growth regulator; heat tolerance; herbicide tolerance; homologous recombination; extreme osmotic condition tolerance; pathogen resistance; pest resistance; yield; photosynthesis; seed oil;

stress resistance.

Cotton cDNA sequence, SEQ ID 6176.

(first entry)

02-DEC-2004

ADR65395;

ADR65395 standard; cDNA; 382 BP

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(GENE-) GENESIS RES & DEV CORP LTD.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention relates to 17880 cotton expressed sequence tags (ESTS;
ACM4520-ACM63099). The ESTS were isolated from cDNA libraries generated
Crom primed or non-primed seeds from variety DP50B, mature seeds from
variety Coker 312 Boswell 96 Field, and androceium tissue, groceium
Crom primed or non-primed seeds from variety wariety
Cromptismed planes, carpel walls and septa from variety
Nucotton33B. The invention also relates to substantially purified
proteins or their fragments encoded by nucleic acid construct
comprising a nucleic acid of the invention. The cotton ESTS are useful as
molecular tags to isolate genetic regions, to isolate genes, to map
genes, to determine gene function and to determining whether genes are
members of a particular gene family. The nucleic acid molecules may be
used for isolating a variety of agronomically significant genes
used for isolating a variety of agronomically significant genes
                                                               926
                                                                                        312
                                                                                                                   986
               866
                                                                                                                                          313 crcrircracececrircraceaeeccrracaacrearcaaecaaaeaaaaaarecaaere 372
                                                                                                                                                                                                                                                                                                                                                                     Cotton; plant; EST; expressed sequence tag; transgenic plant; gynoecium; variety Nucotton33B; library in3B329; molecular tag; molecular marker; genetic mapping; molecular mapping; seed germination; plant growth; plant quality; plant yield; plant breeding; tissue printing; ss.
                                                                                                                                                                                                                                                                                                                                           Cotton gynoecium tissue EST Clone ID: LIB3829-012-Q6-N6-G10, SEQ:13614.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New isolated nucleic acid molecule that encodes a plant protein or its fragment, useful for isolating a variety of agronomically significant genes associated with plant growth, quality or yield, and as molecular
                                   193 GCAGAAGACAGTGTGGCTAAAAGGGTTTTGCGTGAACATGTTCGTGAATCGCTTGGAGTG
                                                               CGGAGTGAGGATCTCCTGTTTGCAATAATAAACAGTGTATCACGAGGAAAGGGACAAGAC
                                                                                                                  TTATTTCTTCAAGCATTTTATCAGGCTTTGCAGCTCATCCAACACGAGAAACTTAAAGTG
             GCTGAAGACAATGTCGCAAGAGAGTCCTACGGGAACATATTCGTGAATCCCTTGGAGTA
                                                                                        cecaareacearrracrerrrecerraaraaaraererreceaeeaaaaeeecaeear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 1; SEQ ID NO 13614; 34pp; English.
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                                                                                                                                                                                                                                                             ACN58833 standard; cDNA; 514 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    12-DEC-2001; 2001US-00021323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             14-DEC-2000; 2000US-0255619P
                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Deikman J, Feng PCC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DEIKMAN J.
FENG P C C.
FINCHER K L.
ZIEGLER T E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2004-479808/45.
                                                                                                                                                                                                                                                                                                                                                                                                                                      Gossypium hirsutum
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                                                                                                                                                                                               CC 374
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(FENG/) I
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To Maria Con

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links in metabolic and catabolic pathways. The nucleic acid molecules are also useful for identifying genes important in initiating and maintaining seed germination or that may be used to matigate stresses encountered during seed germination. The BSTs additionally enable the acquisition of promoters and cis-regulatory elements which will be useful to express agronomically significant genes in these tissues and/or other tissues, and also permits the acquisition of molecular markers useful in breeding schemes, genetic and molecular mapping, and in cloning of agronomically significant genes. The nucleic acid molecules are further useful for detecting the expression level or pattern of a protein or mRNA and for detecting the presence or quantity of a protein by tissue printing. The present sequence represents a specifically claimed EST isolated from a cotton variety Nucottoni3B gynoecium tissue cDNA library (LIB3829). The sequence data for this patent did not form part of free printed from the use opecification, but was obtained in electronic formed directly from the US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1221
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          specification, but was obtained in electronic format directly from the US patent office at seqdata.uspto.gov/sequence.html?DocID=US20040123340
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1162 AGGCCCGTGGAGAATGCTTTGGAAGGATAACAATTGAAGCAATGGCATTCAAGTTGCCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1222 TATTGGGCACGCTGCTGGAGGGACCACGGAGATCGTCCTGGACGGCTCGACTGGCCTTC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GCCACGCCGAGCAGAGGGTCTCCATGGGGGAAAAGGGGCTATGGCAGGGTGAAGGAAATGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              514 AGGGACGGGGAGAATGCTTTGGACGGATAACAATCGAAGCAATGGCATTTCAGTTGCCTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 9.3%; Score 158.6; DB 13; Length 514; Best Local Similarity 70.4%; Pred. No. 5e-34; Matches 212; Conservative 0; Mismatches 89; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Seguence 514 BP; 136 A; 124 C; 90 G; 164 T; 0 U; 0 Other;
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New recombinant DNA constructs useful in the field of biochemistry and genetics, and in particular for producing transgenic plants with improved biological characteristics.

Claim 1; SEQ ID NO 3734; 14pp; English.

18-DEC-2003; 2003US-00739930. 28-APR-2003; 2003US-00424599. 28-APR-2003; 2003US-00425115.

(KOVA/) KOVALIC D K.

WPI; 2004-757369/74.

Kovalic DK;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       687
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              259
                                                                                                                                                                             Sequences AAA31040-A32093 represent novel plant microsatellite sequences and associated flanking species. The sequences comprise a central core repeat sequence, especially selected from the sequences AAA32094-A32096 with left and right flanking sequences. The polynuclectide sequences can be used in the detection of DNA polymorphisms, in genome mapping, in positional cloning of genes, in variety identification and in evaluations, cultivars, species and species between plant tissues, populations, cultivars, species and species groups. They may also be used to design hybridization probes for oligonucleotide fingerprinting and library screening and to design primers for microsatellite-primed PCR. Microsatellite markers are useful to locate specific economically useful genes in plant genomes
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                                                                                                microsatellite markers and associated flanking species for the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TGCGTGGGCATTACTTTAAGGTTGAATATGTCAAACATCTTCCCTTTGTTGCTGGAGCCA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 284 BP; 97 A; 48 C; 73 G; 66 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       69;
                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 154.6; DB 3
Pred. No. 4.9e-33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Mismatches
                                                                                                                   detection of polymorphic genetic markers.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 284
                               Glenn M;
(FLET-) FLETCHER CHALLENGE FOREST LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 260 CAGAAGATAATGTGGCCAAAAGGGT
                                                                                                                                                   Claim 1; Page 106; 392pp; English.
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                                 Bloksberg LN,
                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
9.1%;
Best Local Similarity 74.0%;
Matches 196; Conservative (
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                                                                  WPI; 2000-116958/10.
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                               Havukkala IJ,
                                                                                                   New plant
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28-OCT-2004

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The invention relates a recombinant DNA construct comprising a polymeptide with any of 5544 amino acid sequences (CDNAs SEO INO: 1-5544) and encoding a polymeptide with any of 5544 amino acid sequences (SEO IN No: 5454-1108). The CDNAs and proteins are from corn, soybean, which and rape but the specification does not indicate which sequences is derived from which organism. Also included is a method of proteins at a method of sequences is derived from which organism. Also included is a method of proteins a plant having an improved property, comprising transforming a plant with a recombinant DNA construct comprising transforming a plant with a recombinant DNA construct comprising transforming a plant with a plant cell operably joined to a polymucleotide encoding polant with a plant tell polant cells by modification of the cell cycle pathway, for improving plant coll tolerance to plant disease, for galactomannan production, for providing increased resistance to plant disease, for improving plant tolerance to plant disease, for improving plant tolerance to extreme osmetic conditions, for improving plant tolerance to extreme pasts, for yield improvement by modification of plant tolerance to extreme pasts, for yield improvement by modification of combination in plants, for light in proving plant tolerance to extreme pasts, for yield improvement by modification of carabohydrate, nitrogen or phosphorus use and/or uptake and for yield improvement by modification of carabohydrate, nitrogen or phosphorus use and/or uptake and for yield improvement by providing improved plant growth and derycopence of phosphorus and and/or content, for yield improvement by modification and for yield improvement by expending improved plant growth and for yield improvement by providing improved plant growth and for yield improvement by providing improved plant growth and for yield improvement by providing improved plant general caracteristics such as increased yield, improved introgen for producing arransferiors of the invention. Note: The s
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1306 TEGECOCTCTTGCAAAGAACATCGTCAGACTCGCAAGCCACGCCGAGCAGAGGGTCTCCA
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57.5%; Pred. No. 1.1e-09;
ive 0; Mismatches 50; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 1964 BP; 671 A; 323 C; 378 G; 592 T; 0 U; 0 Other;
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Matches 104; Conservative
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98US-0090170P

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phosphoglucoisomerase; vacuolar hydrogen translocating-pyrophosphatase; pyrophosphate-dependent fructose-6-phosphate phosphotransferase; invertase; sucrose synthase; hexokinase; fructokinase;
                                                                                          lant; ss; EST; expressed sequence tag; transgenic; sucrose pathway; riose phosphate isomerase; fructose 1; 6-bisphosphate aldolase; ructose 1; 6-bisphosphate; fructose 6-phosphate 2-kinase;
                                                                                                                                                          glucose-6-phosphate 1-dehydrogenase; phosphoglucomutase; UDP; uridine diphosphate-glucose pyrophosphorylase; soybean.
                                                                                                                                                nucleoside diphosphate kinase-kinase; NDP;
                                                                        Soybean sucrose synthase EST #28
                  ADA60128 standard; cDNA; 254 BP
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98US-0074281P.
98US-0074282P.
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98US-0092036P.
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98US-0100672P.
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(FISH/) FISHER D
(LIUJ/) LIU J.
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New maize or soybean enzymes and nucleic acid molecules associated with the sucrose pathway, useful for genome mapping, gene identification and analysis, plant breeding, or preparation of constructs for plant gene

Claim 2; Page; 117pp; English.

The invention relates to a substantially purified nucleic acid molecule (appearing as ADA57847 - ADA60660 that encodes a maize or soybean enzyme or its fragment, associated with the sucrose pathway selected from:

Cor its fragment, associated with the sucrose pathway selected from:

triose phosphate isomerase, fructose 1,6-bisphosphate aldolase, fructose fructose prosphotransferase, invertase, sucrose synthase, taructose-6-phosphate phosphotransferase, invertase, sucrose synthase, caphosphate (DDP) educose pyrophosphate kinase (MDP) kinase, chosphate (UDP) educose pyrophosphotylase. Also included are a substantially purified maize or soybean enzyme (or its fragment) and a transformed plant having a nucleic acid molecule. Also included are a substantially purified antibodies capable of specifically binding to the maize or soybean enzyme, determining a level or pattern of a plant sucrose pathway excepted antibodies capable of specifically binding to the maize or soybean enzyme, determining a level or pattern of a plant sucrose pathway enzyme, determining a mutation in a plant core pathway enzyme, producing a plant containing an overexpressed or reduced level of plant sucrose pathway enzyme in a plant trait. The maize or overexpressed or reduced level of plant sucrose pathway enzyme in a plant trait. The maize or soybean enzymes and nucleic acid molecules are useful for genome mapping, gene identification and analysis, plant breeding, or preparation of constructs for plant gene expression and transgenic plants. The nucleic acid molecules are useful as markers or probes. The present sequence is a soybean BST (expressed sequence tag) from a gene encoding a sucrose cathway enzyme. Note: The sequence data for this patent did not form part

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The invention describes a substantially purified nucleic acid molecule that encodes a maize, soybean or Arabidopsis thaliana transcription factor or its fragment, where the maize or soybean transcription factor is homeobox, HIH, leucine zipper, zinc finger, or other transcription
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 1116 GTGGCCCCTTACTTGGCAGCAATTGATGTGCTTGTTCAGAATTCTCAGGGCCGTGGAGAA 1175
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of the printed specification, but was obtained in electronic format directly from USPTO at segdata.uspto.gov/sequence.html?DocID=20030135870.
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                                                                                                                                                                                                                                                                                                                                                        maize; soybean; Arabidopsis thaliana; transcription factor; homeobox; HLH; leucine zipper; zinc finger; transformed plant; plant; metabolic pathway; mutation detection; polymorphism; plant trait; genome mapping; gene identification; gene analysis; plant breeding; transgenic; ds.
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                                                 Length 254;
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                            Sequence 254 BP; 61 A; 53 C; 68 G; 69 T; 0 U; 3 Other;
                                               Query Match

4.0%; Score 67.4; DB 9;
Best Local Similarity 60.5%; Pred. No. 2.5e-08;
Matches 127; Conservative 0; Mismatches 82;
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New substantially purified nucleic acid molecule that encodes a maize, soybean or Arabidopsis thaliana transcription factor or its fragment, useful for genome mapping, gene identification and analysis or plant
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98US-0099667P
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09-SEP-1998;
16-SEP-1998;
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08-DEC-1998
11-DEC-1998
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09-SEP-1998;
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ranscription factor or its fragment defined above; a substantially purified antibody or its fragment which is capable of specifically binding to the transcription factor or its fragment which is capable of specifically binding to the transcription factor or its fragment above; a transformed plant; a method for determining a level or pattern in a plant cell of a transcription factor in a plant; a method of producing a plant containing an overexpressed protein ore reduced levels of plant containing an overexpressed protein ore reduced levels of plant containing an overexpressed protein ore reduced levels of plant containing an association between a plant trait; and a method of isotating a nucleic acid that encodes a plant transcription factor or its fragment. The nucleic acid molecules, proteins and their fragments are useful for genome mapping, gene identification and analysis, plant breeding, preparation of constructs for use in plant gene expression and transgenic plants. The nucleic acid molecules are useful as markers or probes. This sequence represents a soybean transcription factor polynucleotide.
8X363666666666668888
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Sequence 254 BP; 61 A; 53 C; 68 G; 69 T; 0 U; 3 Other;

1116 GIGGCCCCTTACTTGGCGAGCAATTGATGTGCTTCTTCAGAATTCTCAGGGCCGTGGAGAA 1175 1176 TGCTTTGGAAGGATAACAATTGAAGCAATGGCATTCAAGTTGCCAGTATTGGGCACGGCT 1235 1236 GCTGGAGGGACCACGGAGATCGTCCTGGACGGCTCGACTGGCCTTCTGCATCCTGCTGGG 1295 131 GCTGGAGGAACACAGGAGATTGTTGAGCACAATGTTACAGGTC-TCTTCATCCTGTTGGA 189 11 GITGCCTCACTTTACTCTGCCGCAGAIGTTTATGTTATAAACTCTCAGGGGCTGGGAGAA 70 1; Gaps Query Match
4.0%; Score 67.4; DB 12; Length 254;
Best Local Similarity 60.5%; Pred. No. 2.5e-08;
Matches 127; Conservative 0; Mismatches 82; Indels 1; 1296 AAGGAGGCGTGCCTCTTGCAAAGAAC 1325 190 CATCCGGGGAATCTTGTTCTTGCANAGATC 219 g 셤 셤 ઠે ઠે ઠ ઠે 셤

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995 ACATGCTGTAGTTGTGGGAAGTGATGTTAATGCTCAGACCCAAATTTGAGACTCAGTTACG 1054
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US-09-937-837-1
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125 125 125 125 125 127 127 127 127 127 127 127 127 127 127		3, Application US/09621976 639063 BWANTION: Jobert, S. Giordano, J.Y. Giordano, J.Y. VENTION: BETS and Encoded Human Proteins. NCE: GENSET.054PR2 LICATION NUMBER: US/09/621,976 LIGATION US: 19335 LIGATION US: 19335 LIGATION US: 19335 LEAD OF US: 19335 LIGATION US: 19335 LEAD OF US: 19335 LE	
Sequence Seq		2; 2; XWKTW: : CTGCC:	
		gth 832; Indels GGGACAAG :::::::: KKKKAWWK	
40 7		ns. Length ; Inde RREKKKK RAAAGGGACI RREKKKKK RAAAGGAACI RAGAAACI RGAAACI RGAAACI RGAAACI RGAAACI RGAAACI	;
-623-2 -540-1187 -016-125055 -016-14207 3-840A-2 3-840A-2 3-840A-2 3-91A-1306, -991A-1277 -227C-1 -991A-1277 -198-1 -016-16131 -016-16132 -016-16132 -016-16132 -016-16132 -1016-16132 -1016-16132 -1016-16132 -1016-16132		n Protein DB 3; L 0.0016; hes 128; TCACGAGGA :::: YYMKTYWRW	
-142-623-2 -902-540-118 -949-016-125 -949-016-142 9-103-840A-2 9-103-840A-2 9-103-840A-2 -252-991A-13-252-991A-13 -252-991A-13-252-991A-13-2949-016-161 -949-016-161-161 -949-016-161-161 -949-016-161-161 -949-016-161-161 -949-016-161-161 -949-016-161-161 -949-016-161-161 -949-016-161-161 -949-016-161-161 -949-016-161-161 -949-016-161-161	MENTS	976 B. (ed Human P. 621,976 621,976 Mismatches CAGTGTATCACACA :::::: YWMYWKWYYYM G-CTCATCCAL GYMWWYWGWI	
	ALIGNMENT	ULT 1 CQ-621-976-2813 equence 2813, Application US/09621976 atent No. 6639063 atent No. 6639063 applicant incommittee Gallons APPLICANT: Jobert, S. APPLICANT: Glordano, J.V. TILLE OR INVENTION: ESTS and Encoded Human Proteins FILE REFERENCE: GENSET.054PR2 TILLE REFERENCE: GENSET.054PR2 CURRENT APPLICATION NUMBER: US/09/621,976 CURRENT APPLICATION 1335 LENGTH 832 LENGTH 832 LENGTH 832 LENGTH 832 LENGTH 832 LOCAPION: 235399 OD-621-976-2813 atches 39; CONSERVATHWARKCHTARARACAGTGTATCACGAGAGAAA 2	!
		S/096; rds, r d Enc, R2 US/0 07-21 183; 183; EWKWSI CTTTG	
1905 18551 670689 670689 64403765 4410376 1578 1824 44377 44377 44377 47181 2855 47181 47181 1141 1143 1965		ULT 1 10-621-976-2813 40-621-976-2813 40-618-13, Application US/0962197, Application US/0962197, Application US/0962197, Application US/0962197, Application US/0962197, Applicant Information University of Gardano, J.Y. Applicant: Gardano, J.Y. Experiment Priling Date: 2000-07-21 TURBEN T FILING DATE: 2000-07-21 TURBER OF SEQ ID NOS: 19335 TURBER OF SEQ ID NOS: 19335 TURBER OF SEQ ID NOS: 19335 TOGRANISM: Home Sapiens FEATURE: NAME/KEY: CDS LOCATION: 235399 09-621-976-2813 2.9%; Score est Local Similarity 11.1%; Pred. atches 39; Conservative 183; Miatches 39; Conservative 183; Miatches 39; Conservative 183; Miatches 39; Conservative 183; Miatches 39; CARGCATTTATCAGGCTTTGCAG-0621 Similarity 11.1%; Pred. atches 39; CARGCATTTATCAGGCTTTGCA	
7		plicati 3 ON: Tr, S. dano, J ON: CANDO, J ON: DON: DON: DON: DON: DON: DON: DON:	!
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RESULT 4
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US-09-881-165-4
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1175 ATGCTTTGGAAGGATAACAATTGAAGCAATGGCATTCAAGTTGCCAGTATTG 1226
                  GGTTCATGAGGTCCAAGCTCGTGCTCCTCGTCTCCCATGAGCTCTCCCTC 326
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; Sequence 2, Application US/09130114
; Patent No. 5976807
; GENERAL INFORMATION:
; APPLICANT: Horlick, Robert A.
; APPLICANT: Bomaj, Bassam B.
; APPLICANT: Bombins, Alan K.
; TITLE OF INVENTION: Braryotic Cells Stably Expressing Genes
; TITLE OF INVENTION: From Multiple Transfected Episomes
; FILE REFERENCE: 0867/1D903US1
; CURRENT APPLICATION NUMBER: US/09/130,114
; CURRENT PILING DATE: 1998-08-06
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 2.9%; Score 49.2; DB 3; Length 1926; Best Local Similarity 50.9%; Pred. No. 0.0041; Matches 117; Conservative 0; Mismatches 113; Indels 0
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                                                                                                          Sequence 4, Application US/09249585A
Patent No. 6417002
GENERAL INFORMATION:
APPLICANT: HORLICK, Robert
TITLE OF INVENTION: METHOD FOR MAINTENANCE AND SELECTION OF 1
FILE REFERENCE: 0867/005905
CURRENT APPLICATION NUMBER: US/09/249,585A
CURRENT FILING DATE: 1999-02-11
NUMBER OF SEQ ID NOS: 18
SOFTWARE: Patentin version 3.0
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2.9%; Score 49.2; DB 2; Length 1
Best Local Similarity 50.9%; Pred. No. 0.0042;
Matches 117; Conservative 0; Mismatches 113; Indels
                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: misc_feature; LOCATION: (1)...(1926); OTHER INFORMATION: template strand of EBNA-1 DNA 15-09-249-585A-4
                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Epstein Barr Virus
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ORGANISM: EBNA
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Sequence 54, Application US/10152886

Sequence 54, Application US/10152886

Patent No. 6912470

GENERAL INFORMATION:

APPLICANT: ECOPIA BIOSCIENCES INC.

APPLICANT: Staffa, Alfredo

APPLICANT: Staffa, Alfredo

APPLICANT: Zazopoulos, Emmanuel

TITLE OF INVENTION: GENES AND PROTEINS INVOLVED IN THE BIOSYNTHESIS OF ENEDIYNE RING

TITLE OF INVENTION: STRUCTURES

FILE REFERENCE: 3011-30S

CURRENT APPLICATION NUMBER: US/10/152,886

CURRENT APPLICATION NUMBER: US/10/152,886

SOFTWARE: Patentin version 3.0

SEQ ID NOS: 102

SEQ ID NO 54

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TCGCCGGAGGCCGCGGGCCGGTTCACAACCGGACCCAGCTCCTCCTCCTCCTCGTGG
                                                                                                                     157 CCGTCGCAGCCTCCGCATCCACAGCAGGGTTCCTCCTCCGCGGTGCCCTGCGAGACCCTT
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Pred. No. 0.0084;
0; Mismatches 165; Indels
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Local Similarity 47.3%;
es 148; Conservative
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ORGANISM: Kitasatosporia sp.
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63 ATGGCAAAGACCCCGTCGTTCGCGGTGGCGGCGGTCGCCGGAGGCCGCGGGGCCGGTTCAC 122
                                                                                                                         123 AACCGGACCCAGCTCCTCCTCCTCCTCGTGGCCGTCGCAGCCTCCGCATCCACAGCA 182
                                                                                                                                                                                                                 445 CCAGAATCCGCCGCACTCCCAGACGCCCCCGCGTCGACGCGCCAACCCGATCCAAGACA 504
                                                                                                                                                                                                                                                                                                      505 CCCGCGCAGGGGCTGGCCAGAAAGCTGCACTTTAGCACCGCCCCCCAAACCCCGACGCG 564
                                                                                                                                                                                                                                                                                                                                                 CTCAACACCGCCGTCGCCAGCGGGAGTCCCCTCGGGTTCATGAGGTCCAAGCTCGTGCTC 302
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TCGGCTCGAGTTTGATCCGAGCCCACAGTCTCTCTCGGGCCCACCGCGTCCGACCGGCG 62
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; Mismatches 163;
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Pred. No. 0.0054;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY AGENT INFORMATION:
NAME: Vincent, Matthew P.
REGISTATION NUMBER: 36,709
REFERENCE/DOCKET NUMBER: MIV-069.03
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LLP
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Patent No. 6495526
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
ADDRESSEE: FOLEY, HOAG & ELIOT
STREET: One Post Office Square
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: 617-832-7000
INFORMATION FOR SEQ ID NO: 13:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Gyuris, Jeno
APPLICANT: Lamphere, Lou
APPLICANT: Beach, David
TITLE OF INVENTION: INHIBH:
TITLE OF INVENTION: RELATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ZIP: 02109-2170
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy A'
COMPUTER: IPP'
COMPUTER: IPP'
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Best Local Similarity
Matches 146; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     124 ACCGGACCCAGCTCCTCCTCCTCCTCGTGGCCGTCGCAGCCTCCGCATCCACAGCAG 183
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                                                                                  APPLICANT: WARD, MICHAEL
APPLICANT: WOODARD, SUSAN
TITLE OF INVENTION: METHOD OF INCREASING RECOVERY OF HETEROLOGOUS ACTIVE
TITLE OF INVENTION: ENZYMES PRODUCED IN PLANTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 76 cceedgaccecarcaacaccerecececececearcaccarcreceaegcceecrreacc
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Description of Artificial Sequence: Ndel-EcoRl fragment
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2.8%; Score 48.4; DB 3; Length 1082; 53.1%; Pred. No. 0.0052; tive 0; Mismatches 91; Indels 0
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Pred. No. 0.0054;
0; Mismatches 163; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Benson, John
APPLICANT: Kasukawa, Hiroaki
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATING
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATING
TITLE OF INVENTION: PAPILLCMAVIRUS-INPECTED CELLS
FILLS REFERENCE: HWV-041.01
CURRENT APPLICATION NUMBER: US/09/347,504
CURRENT FILING DATE: 1999-07-02
NUMBER OF SEQ ID NOS: 79
                                                                                                                                                                FILE REFERENCE: 10032R
CURRENT APPLICATION NUMBER: US/09/881,165
CURRENT FILING DATE: 2001-06-14
PRIOR APPLICATION NUMBER: 60/211,732
PRIOR FILING DATE: 2000-06-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 11, Application US/09347504
Patent No. 6399075
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                      TYPE: DNA ORGANISM: Artificial Sequence
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LEWOTH: 912
TYPE: DNA
ORGANISM: Artificial Sequence
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Best Local Similarity 47.2%;
Matches 146; Conservative
                BAILEY, MICHELE
GASTEL, FRANS VAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      304 TCGTCTCCCATGAG 317
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                                                                                                                                                                                                                                                                            NUMBER OF SEQ ID NOS: 5
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 4
LENGTH: 1082
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Best Local Similarity 53.1
Matches 103; Conservative
                                                         WANG, HUAMING
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                                                                              APPLICANT:
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                                                         APPLICANT
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Length 912; IndelB

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243 CTCAACACCGCCGTCGCCAGCGGGAGTCCCCTCGGGTTCATGAGGTCCAAGCTCGTGCTC 302
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Facture No. 6773920

GENERAL INFORMATION:

APPLICANT: INVITERGEN CORPORATION

APPLICANT: BENNETT, Robert

TILLE OF INVENTION: DELIVERY OF FUNCTIONAL PROTEIN SEQUENCES

TILLE OF INVENTION: DELIVERY OF FUNCTIONAL PROTEIN

TILLE OF INVENTION: DELIVERY OF FUNCTIONAL PROTEIN

TILLE OF INVENTION: DELIVERY OF FUNCTIONAL PROTEIN

TILLE OF INVENTION: DELIVERY OF 9937,837

CURRENT FILING DATE: 2001-09-28

PRIOR APPLICATION NUMBER: DCT/USOO/08571

PRIOR PLING DATE: 2000-03-31

PRIOR PLING DATE: 1999-03-31

NUMBER OF SEQ ID NOS: 21
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Patent No. 6200577

GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: THERPESVIRAL ALENTS AND ASSAYS;
TITLE OF INVENTION: THERPESVIRAL ALENTS AND ASSAYS;
TITLE OF INVENTION: THERPESVIRAL ALENTS AND ASSAYS;
TILE REFERENCE: P10189C

CURRENT APPLICATION NUMBER: US/09/230,421

CURRENT FILING DATE: 1999-01-25

NUMBER OF SEQ ID NOS: 14

SOFTWARE: FASTERQ for Windows Version 3.0
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US-09-230-421-1
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Fatent No. 667354
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APPLICANT: SCHEIFLINGER, F.
APPLICANT: FALKNER, F. G.
TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
CORRESPONDENCE: 52
CORRESPONDENCE ADDRESS:
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CITY: Alexandria
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/232,463
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS.
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REFERENCE/DOCKET NUMBER: 30
TELECOMMUNICATION INFORMATION:
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FILING DATE: 26-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,7
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INFORMATION FOR SEQ ID NO:
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LENGTH: 7218 base pair
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CLONE: pTZgpt-F1s
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Best Local Similarity
Matches 12; Conserv
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APPLICANT: BENNETT, Robert
TITLE OF INVENTION: DELIVERY OF FUNCTIONAL PROTEIN SEQUENCES
FILE REFERENCE: INVIT1280-1
                                                                                                                                                                                        Pred. No. 0.015;
0; Mismatches 163; Indels
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Pred. No. 0.015;
0; Mismatches 163;
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US-09-937-837-2
                                                                                                                                                                        Score 48.2;
Pred. No. 0.
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NUMBER OF SEQ ID NOS: 21
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 2
LENGTH: 6420
SOFTWARE: PastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION NUMBER: US/09/937,837
CURRENT FILING DATE: 2001-09-28
PRIOR APPLICATION NUMBER: PCT/US00/08571
PRIOR FILING DATE: 2000-03-31
PRIOR APPLICATION NUMBER: 60/127,467
                                                                       ORGANISM: Artificial Sequence
FEATURE:
J. OTHER INFORMATION: vector pVP22/Myc-His
US-09-937-837-1
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Patent No. 6773920
GENERAL INFORMATION:
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Best Local Similarity 47.2%;
Matches 146; Conservative
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Best Local Similarity 47.2%;
Matches 146; Conservative
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                                                                                                                                                                                                                               Query Match
2.7%; Score 46.8; DB 2; Length 4:
Best Local Similarity 48.8%; Pred. No. 0.095;
Matches 126; Conservative 0; Mismatches 132; Indels
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Patent No. 6008013

GENERAL INPORMATION:
TITLE OF INVENTION: CHONDROCYTE PROTEINS
FILE REFERENCE: 176/60091

CURRENT APPLICATION NUMBER: US/08/680,506C

CURRENT PILING DATE: 1996-07-08

BARLIER PILING DATE: 1996-07-08

BARLIER PILING DATE: 1996-07-05

WUMBER OF SEQ ID NOS: 18

SOFTWARE: PATENTIN VEY: 2.0
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LOCATION: 31232..36067
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36249..41774
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ORGANISM: Gallus gallus
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Matches 97; Conserv
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US-08-804-227C-1
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US-08-680-506-5
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                                          FEATURE
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                                          GGTCGCCGGAGGCCGCGGCCGGTTCACAACCGGACCCAGCTCCTCCTCCTCCTCGT 154
                                                                                                                                                                                                              155 GGCCGTCGCAGCCTCCGCATCCACAGCAGGGTTCCTCCTCCGCGGTGCCCTGCGAGACCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
APPLICANT: DeHoff, Bradley S.
APPLICANT: Mustces, Stuart A.
APPLICANT: Knoteck, Paul R., Jr.
APPLICANT: Sutton, Kimberly L.
TITLE OF INVENTION: POLYKETIDE SYNTHASE GENES NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: THOMAS G. PLANT 1501
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   335 TCCACTTTTACTGATGGAATTAGCATTTCTTCT 367
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM COMPATIABLE
OPERATING SYSTEM: MS-DOS
SOFTWARE: ASCI(DOS) Text only
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/804,227C
TITING DATE: REBILARY 21, 1997
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ATTORNEY/AGENT INFORMATION:
NAME: Plant, Thomas, G.
REGISTRATION NUMBER: 35,784
REFERENCE/DOCKET NUMBER: X-8231
TELECOMMUNICATION INFORMATION:
TELEPHONE: 317-276-2459
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
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STREET: LILLY CORPORATE CENTER
CITY: INDIANAPOLIS
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FEATURE:
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LOCATION:
FEATURE:
NAME/KEY:
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US-09-902-540-7944

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Sequence 7944, Application US/09902540

Sequence 7944, Application US/09902540

Patent No. 683347

GENERAL INFORMATION:

APPLICANT: Goldman, Barry S.

APPLICANT: Gladen, Eaven C.

APPLICANT: Hinkle, Gregory J.

TILE REFERENCE: 38-10(15849)B

CURRENT APPLICATION UNDBER: US/09/902,540

CURRENT TILING DATE: 2001-07-10

PRIOR FILING DATE: 2000-07-10

NUMBER OF SEQ ID NOS: 16825

SEQ ID NO 7944

LENGTH: 1239
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1299 GAGGGCGTGCCTCTTGCAAAGAACATCGTCAGACTTCGCAAGCCACGCCGAGCAGAGG 1358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1359 GTCTCCATGGGGGAAAAGGGCTATGGCAGGGTGAAGGAAATGTTCATGGAGCACCACATG 1418
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         964 TTGGGCCTGCCCATCATGGAGGCCATGCCTGCCGTGCTGCTGGTGGTGGCCGCG 1023
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1084 CCCCGC-----ACCCTGGCGGACAAAGCTGGAGACCGTGGCGCGCGCGGCGCCCCAGGAGGCC 1137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1138 caccescricionicados de constante en 1197 cacestrados de 1197 de cacestrados de 1197 de 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          6; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 2.7%; Score 46.6; DB 3; Length 1239; Best Local Similarity 51.3%; Pred. No. 0.018; Matches 137; Conservative 0; Mismatches 124; Indels 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1419 GCTGAGAGGATCGCGGCGGTGTTGAAG 1445
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1198 GCGGACATGCTCGCGCAGATGCTCCAG 1224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Search completed: March 17, 2006, 04:44:36 Job time : 334 secs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: DNA ORGANISM: Myxococcus xanthus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-09-902-540-7944
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## 5.1.7 Biocceleration Ltd. GenCore version Copyright (c) 1993 - 2006

nucleic search, using sw model OM nucleic

March 17, 2006, 04:44:58; Search time 1454 Seconds (without alignments) 9679.836 Million cell updates/sec Run on:

US-09-938-294-2 1702

1 attoggetcgagtttgatcc......gaggagatttcaatcttagt 1702 Sequence:

IDENTITY_NUC Gapop 10.0 , Gapext 1.0 Scoring table:

9793542 seqs, 4134689005 residues

Total number of hits satisfying chosen parameters:

length: 0 length: 2000000000 Minimum DB Maximum DB

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

cgn2_6/ptodata/1/pubpina/US07_pruBCOMB.seq:*
cgn2_6/ptodata/1/pubpina/US08_BruBCOMB.seq:*
cgn2_6/ptodata/1/pubpina/US08_BruBCOMB.seq:*
cgn2_6/ptodata/1/pubpina/US09_PuBCOMB.seq:*
cgn2_6/ptodata/1/pubpina/US10_PuBCOMB.seq:*
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cgn2_6/ptodata/1/pubpina/US10_PuBCOMB.seq:*
cgn2_6/ptodata/1/pubpina/US10_PuBCOMB.seq:* Published_Applications_NA_Main:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description	Sequence 3707, Ap	Sequence 103279,	Sequence 39774, A	Sequence 12116, A	Sequence 9892, Ap	Sequence 64438, A	Sequence 6175, Ap	Sequence 6035, Ap	Sequence 6035, Ap	Sequence 6078, Ap	Sequence 6078, Ap		133, A	1357	Sequence 3627, Ap	Sequence 77966, A	Sequence 6176, Ap	Sequence 163392,	Sequence 53829, A	Sequence 13614, A	Sequence 101, App	٠.	Sequence 53164, A
ID	US-10-425-114-3707	US-10-425-115-103279	US-10-437-963-39774	US-10-767-701-12116	US-10-767-701-9892	US-10-424-599-64438	US-10-767-795-6175	US-09-923-876-6035	US-09-923-876-6035	US-09-923-876-6078	US-09-923-876-6078	US-10-767-795-3626	US-09-770-152-133	US-10-021-323-13572	US-10-767-795-3627	US-10-424-599-77966	US-10-767-795-6176	US-10-425-115-163392	US-10-424-599-53829	US-10-021-323-13614	US-10-062-727-101	US-10-425-115-173887	US-10-424-599-53164
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Length	1647	1853	1449	1048	667	2395	1094	276	276	257	257	948	583	625	625	606	382	345	537	514	284	396	665
& Query Match	96.8	93.5	61.3	45.6	36.1	26.0	25.0	15.4	15.4	15.1	15.1	14.4	13.7	13.3	13.3	12.8	12.3	11.6	10.6	9.3	9.1	8.7	8.5
Score	1647	1591.8	1042.6	776.4	614.2	441.8	426.2	262	262	257	257	244.8	233	227	227	217.2	210	196.6	179.6	158.6	154.6	148.6	144.4
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48394, A	3734, Ap	2282, Ap	2871, Ap	6433, Ap	27859, A	103198,	60378, A	250, App	5250, Ap	62523, A	10984, A	175665,	40423, A	170475,	99654, A	62522, A	12, Appl	1, Appli	55246, A	55247, A	242, App	
Sequence	Sequence		Sequence	Sequence	Sequence	Seguence	Sequence		Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence		Sequence	Sequence	Sequence	Sequence	Sequence	
 US-10-424-599-48394	US-10-739-930-3734	US-09-237-183A-2282	US-09-922-293-2871	US-10-437-963-6433	US-10-425-115-27859	US-10-424-599-103198	US-10-437-963-60378	US-10-128-714-250	US-10-128-714-5250	US-10-437-963-62523	US-10-767-701-10984	US-10-425-115-175665	US-10-437-963-40423	US-10-425-115-170475	US-10-437-963-99654	US-10-437-963-62522	US-10-211-028-12	US-10-211-028-1	US-10-437-963-55246	US-10-437-963-55247	US-10-335-053-242	
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100	74	67.4	67.4	57.6	56.8	53.6	52.8	52.4	52.4	52	51.6	51.4	51.2	50.4	50.4	50.4	50.4	50.4	20	20	20	
24	25	56	27	28	53	30	31	32	33	34	35	36	37	38	9 6	40	41	42	43	44	45	
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## ALIGNMENTS

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56 ACCGGCGATGGCAAAGACCCCGTCGTTCGCGGTGGCGGCGGTCGCCGGGCCCGCGGGCC 115
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Cao, Yongwei Tritz OF INVENTION: Nucleic Acid Molecules and TITLE OF INVENTION: Nucleic Acid Molecules and TITLE OF INVENTION: Plants and Uses Thereof fo File Reperrors: 38-21(53313) B CURRENT APPLICATION NUMBER: US/10/425,114 CURRENT APPLICATION NUMBER: 2003-04-28 NUMBER OF SEQ ID NOS: 73128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    96.8%; Score 1647; D
100.0%; Pred. No. 0;
ative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; FEATURE:
; OTHER INFORMATION: Clone ID: 700335931_FLI
US-10-425-114-3707
Sequence 3707, Application US/10425114
Publication No. US20040034888A1
GENERAL INFORMATION:
APPLICANT: Liu, Jingdong
                                                                                                                                                                                                                                     Zhou, Yihua
Kovalic, David K.
Screen, Steven E
Tabaska, Jack E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity
Matches 1647; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: DNA ORGANISM: Zea mays
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   116
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     241 TAAACAGTGTATCACGAGGGAAGGGACAAGACTTATTTTTTATCAGGGTT 300
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                                   RESULT 4

US-10-767-701-12116

US-10-767-701-12116, Application US/10767701

Publication No. US20040172684A1

GENERAL INFORMATION:

APPLICANT: Kovalic, David K.

APPLICANT: Cao, Yongwei

TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated V TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated V TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement

FILE REFERENCE: 38-21(53535)8

CURRENT APPLICATION NUMBER: US/10/767,701

CURRENT FILING DATE: 2004-01-29

NUMBER OF SEQ ID NOS: 63128
                                                                                                                                                                                                                                                                                                                                                                                                                                    acctggggaatagtaaagaactaatggaagttgctgaagacaatgtggcaagaagagtcc
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CAATTGATGTGCTTGTTCAGAATTCTCAGGGCCGTGGAGAATGCTTTGGAAGGATAACAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TTGAAGCAATGGCATTCAAGTTGCCAGTATTGGGCACGGCTGCTGGAGGGACCACGGAAA
                                                                                                                                                                                                                                                                                                                                                                                   715 ATTGGAATAGCAGGACTAGCGATCGCCTGAAAATACAGATGCCACAAACTTATGTTGTTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ACCTGGGGGAATAGTAAAGAACTAATGGAAGTTGCTGAAGATAATGTCGGAAGAAGAGAGTCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TGCAGCTCATCCAACACGAGAAACTTAAAGTGCCTAGAATACATGCTGTAGTTGTGGGAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  301 recaecrcarccaacaccagaaacraaaagreccracaarecarecraragricregeaa
                                                                                                                                                                                                                                                                                                                                                                    655 ATGICAAACAICTICCCTITGTIGCTGGAGCCATGATTGATTCTCATACAACGGCTGAGT
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                                                                                                                                                                                                                                                                                                                    Length
                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                       ; OTHER INFORMATION: Clone ID: SORBI-28MAY03-CLUS10968_1
US-10-767-701-12116
                                                                                                                                                                                                                                                                                                                  Score 776.4; DB 7;
Pred. No. 4.4e-228;
0; Mismatches 36;
                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 95.7%;
Matches 798; Conservative
                                                                                                                                                                                                                                           TYPE: DNA
ORGANISM: Sorghum bicolor
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0y         1315 TTGCAAAGAACATCGTCACACTCGCAAGCCACCCACCACACACA	Baser Local Similarity   36.1%;   Score 614.2;   DB 7;   Length 667;

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Sequence 6035, Application US/09923876
Patent No. US20020013958A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Lalgudi, Raghunath V.
APPLICANT: Kamigaki, Laura Y. (Ito)
APPLICANT: Sharman, Bradley W.
TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM CORN SEEDLING
FILE REFERENCE: PL-0012-1 CON
CURRENT APPLICATION NUMBER: US/09/923,876
CURRENT FILING DATE: 2001-08-06
PRIOR APPLICATION NUMBER: 09/298,329
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Sequence 6175, Application US/10767795
Publication No. US20040181830A1
Sequence 6175, Application Sequence 6175, Application No. US20040181830A1
SPELICANT: Covalic, David K. APPLICANT: Zhou, Yingwei
APPLICANT: Britis OF INVENTION: Plants and Uses Thereof For Plant Improvement
TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement
TITLE OF INVENTION: US/10/767,795
CURRENT FILING DATE: 2004-01-30
CURRENT FILING DATE: 2004-01-30
SEQ ID NO 6175
LENGTH: 1094
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Pred. No. 6.1e-120;
0; Mismatches 348;
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Matches 666; Conservative
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US-10-767-795-6175
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publication No. US20030237110A9

publication No. US20030237110A9

GENERAL INFORMATION:

APPLICANT: Lalgudi, Raghunath V.

APPLICANT: Lalgudi, Radhunath V.

APPLICANT: Sherman, Bradley K.

TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM CORN SEEDLING

FILE REPERENCE: PL-0012-1 CON

CURRENT APPLICATION NUMBER: US/09/923,876

CURRENT PILING DATE: 1999-04-21

PRIOR FILING DATE: 1999-04-21

PRIOR FILING DATE: 1999-04-21

PRIOR FILING DATE: 1999-05-05

NUMBER OF SEQ ID NOS: 6332

SOFTWARE: PERL PROGram

SEQ ID NO 6035

LENGTH: 276
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OTHER INFORMATION: Incyte ID No. US20020013958A1 700458234H1
                                                                                                                                                                                                                                                                                             Length 276;
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Pred. No. 1.3e-69;
0; Mismatches 1;
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LOCATION: 200, 275

: OTHER INFORMATION: a, t, c, g, or other

US-09-923-876-6035
PRIOR FILING DATE: 1999-04-21
PRIOR APPLICATION WUMBER: 60/085,331
PRIOR FILING DATE: 1998-05-05
NUMBER OF SEQ ID NOS: 6332
SOFTWARE: PERL PROGRAM
SEQ ID NO 6035
LENGTH: 276
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99.3%;
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Best Local Similarity 99.3
Matches 273; Conservative
                                                                                                                                     ORGANISM: Zea mays
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ORGANISM: Zea mays
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DB 3; Length 276;

15.4%; Score 262;

Query Match

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APPLICANT: Kamigaki, Laura Y. (Itc)
APPLICANT: Kamigaki, Laura Y. (Itc)
APPLICANT: Sherman, Bradley K.
FITLE OF INVENTION: POLYNUCLECTIDES AND POLYPEPTIDES DERIVED FROM CORN SEEDLING
FILE REFERENCE: PL-0012-1 CON
CURRENT APPLICATION NUMBER: US/09/923,876
CURRENT FILING DATE: 2001-08-06
PRIOR APPLICATION NUMBER: 09/298,329
PRIOR FILING DATE: 1999-04-21
PRIOR FILING DATE: 1998-05-05
NUMBER OF SEQ ID NOS: 6332
SOFTWARE: PERL PROGram
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                                                                                                                                                                                              GTTCA 1153
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                                1; Gaps
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; OTHER INFORMATION: Incyte ID No. US20020013958A1 700458322H1
US-09-923-876-6078
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Pred. No. 4.2e-68;
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     1.3e-69;
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100.0%; Pred. No. ...
0; Mismatches
                                0; Mismatches
  Pred. No.
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Patent No. US20020013958A1
GENERAL INFORMATION:
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  99.38;
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Best Local Similarity 99.39
Matches 273; Conservative
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Best Local Similarity
Matches 257; Conserv
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ORGANISM: Zea mays
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                                                                                                                              Gaps
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                                                                                 Length 948;
                                                                                    Score 244.8; DB 8; Length
Pred. No. 5.7e-64;
0; Mismatches 157; Indels
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TITLE OF INVENTION: Expressed Sequences of Arabidopsis
TITLE OF INVENTION: Lhaliana
FILE REFERENCE: 2025US (PARA-014PRV)
CURRENT APPLICATION NUMBER: US/09/770,152
              , OTHER INFORMATION: Clone ID: GOSHI-09MAY01-C6051_1
US-10-767-795-3626
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Matthew, Abraham V.
Ledford, Brooke L.
Woessner, Jeffrey P.
Haas, William David
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Rameaka, Joshua G.
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Hamilton, Carol M
Price, Jennifer L
Raines, Tracy M.
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                                                                                                                              352; Conservative
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Hoffman, Neil
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                                                                                    Query Match
Best Local Similarity
Matches 352; Conserv
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US-09-770-152-133/c
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yequence 6078, Application US/09923876
yequence 6078, Application No. US20030237110A9
GENERAL INFORMATION:
APPLICANT: Lalgudi, Raghunath V.
APPLICANT: Kamigaki, Laura Y. (Ito)
APPLICANT: Sherman, Bradley K.
TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM CORN SEEDLING
FILE REFERENCE: PL-0012-1 CON
CURRENT APPLICATION NUMBER: US/09/923,876
CURRENT APPLICATION NUMBER: 09/298,329
PRIOR FILING DATE: 1999-04-21
PRIOR FILING DATE: 1999-04-21
PRIOR FILING DATE: 1999-05-05
NUMBER OF SEQ ID NOS: 6332
SOFTWARE: PERL PROGRAM
SEQ ID NO 6078
LENGTH: 257
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Publication No. US20040181830A1
GENERAL INFORMATION:
APPLICANT: Kovalic, David K.
APPLICANT: Cao, Yongwei
APPLICANT: Zhou, Yihua
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement
FILE REFERENCE: 38-21(53534)B
CURRENT APPLICATION NUMBER: US/10/767,795
CURRENT APPLICATION NUMBER: 2004-01-30
NUMBER OF SEQ ID NOS: 117596
SEQ ID NO 3626
LENGTH: 948
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; OTHER INFORMATION: Incyte ID No. US20030237110A9 700458322H1
US-09-923-876-6078
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
15.1%; Score 257; DB 3; Length 257;
Best Local Similarity 100.0%; Pred. No. 4.2e-68;
Matches 257; Conservative 0; Mismatches 0; Indels
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    241 GGCCTTCTGCATCCTGC 257
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ORGANISM: Zea mays
                                                                                        US-09-923-876-6078
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FEATURE:
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APPLICANT: Fincher, Karen L.
APPLICANT: Ziegler, Todd E.
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With TITLE OF INVENTION: Plants
FILE SPERENCE: 38-21(52274)B
CURRENT APPLICATION NUMBER: US/10/021,323
CURRENT FILING DATE: 2001-12-12
PRIOR APPLICATION NUMBER: US 60/255, 619
PRADE FILING DATE: 2000-12-14
                                                                                                                                                                                                                                                                                                                                                                                                       1023 AATGCTCAGACCAAATTTGAGACTCAGTTACGTGACTTTGTGGTGAAGAACACGATTCAT 1082
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1083 GACCGTGTCCATTTTGTGAACAAGACATTGGCAGTGGCCCCTTACTTGGCAGCAATTGAT 1142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1263 GACGGCTCGACTGGCCTTCTGCATCCTGCTGGGAAGGAGGGCGTGGCGCTCTTTGCAAAG 1322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1323 AACATCGTCAGACTCGCAAGCCACGCCGAGCAGAGGTCTCCATGGGGGAAAAGGGCTAT 1382
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1383 GGCAGGGTGAAGGAAATGTTCATGGAGCACCACATGGCTGAGAGGATCGCGGGGGTGTTG 1442
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   448 AACTTTGTCCACTTCGTCAACAAAACTCTAACCGTAGCACCATATATAGCAGCCATAGAC 389
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       388 GTTCTTGTCCAAAACTCCCAAGCCAGGAGAATGCTTTGGGAGAATAACAATCGAAGCC 329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         328 ATGGCCTTTAAGCTACCTGTACTTGGTACTGCAGCCGGAGGAACAATGGAGATTGTAGTG 269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             268 AATGGAACGACTGGTCTGTTACATAGTGCAGGGAAAGAAGAGGGTGATACCTCTCGCCAAG 209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           208 AACATAGTGAAGTTGGCGACGCAAGTTGAGTTACGGCTGAGAATGGGAAAAAATGGGTAT 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 8
                                                                                                                                                                                                                                                                                                                                                           568 ATCAAAGAGAAGAAACTTCAGGTACCAACAATGCATGCAGTAGTAGTAGTAGGAAGCGACATG
                                                                                                                                                                                                                                                                                                                                                                                                                                               1203 ATGGCATTCAAGTTGCCAGTATTGGGCACGGCTGCTGGAGGGACCACGGAGATCGTCCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               148 GAGAGAGIAAAAGAGAIGITITIGGAACATCATAIGICACATCGAATAGCTTCGGTACTC
                                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                                                 Length 583;
                                                                                                                                                                                                                             Score 233; DB 3; Length 58
Pred. No. 1.8e-60;
0; Mismatches 170; Indels
                                                                                                                                                                                                                                                                                                                     963 ATCCAACACGAGAAACTTAAAGTGCCTAGAATACATGCTGTAGT
                                                         NUMBER OF SEQ ID NOS: 999
SOFTWARE: PastSEQ for Windows Version 4.0
SEQ ID NO 133
LENGTH: 583
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1443 AAGGATGTCCTGAGGAAATCACAGG 1467
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 13572, Application US/10021323
Publication No. US20040123340A1
GENERAL INFORMATION:
APPLICANT: Deikman, Jill
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAAGAAGTCTTGCAACACGCAAAGG
CURRENT FILING DATE: 2001-01-26
PRIOR APPLICATION NUMBER: 60/178,503
PRIOR FILING DATE: 2000-01-27
                                                                                                                                             ; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-09-770-152-133
                                                                                                                                                                                                                                 Query Match
Best Local Similarity 66.3%;
Matches 335; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: DNA
ORGANISM: Gossypium hirsutum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-10-021-323-13572
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LENGTH: 625
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Associated With
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             379 ACTGATGAAGTAATATAGTTTTAGAACATAAGATGTTGGACAGAGGAGGAGGGTTTTTC 438
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            599
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CCGAAGATTTTGTGTGGATCCATGAAATGCGTGGGCATTACTTTAAGGTTGAATATGTC 659
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                                                                                                                                                                                                                                                               199 GCCCGCAGATCGCTGCTAAAGCCGAGTCCACTCAGTTTCATGAAGTCCAAGATTGTT 258
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                                                                                                                                                                                                                                                                                                                                                                                    259 cracregrereccaceaecrerecerricregregaecarrerrerrearesaecrasea
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TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement
FILE REFERENCE: 38-21(53534)B
CURRENT APPLICATION NUMBER: US/10/767,795
CURRENT FILING DATE: 2004-01-30
NUMBER OF SEQ ID NOS: 117596
SEQ ID NO 3627
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                                                                                            Length 625;
                                                                                         Score 227; DB 7; Length 62
Pred. No. 1.4e-58;
0; Mismatches 125; Indels
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, OTHER INFORMATION: Clone ID: LIB3829-012-06-K6-G10 US-10-021-323-13572
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Pred. No. 1.4e-58;
); Mismatches 125;
                                                                                                                                                                                                          GCCCTCAACACCGCCGTCGCCAGCGGGAGTCCCCTCGGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; Sequence 3627, Application US/10767795; Publication No. US20040181830A1; GENERAL INFORMATION:
APPLICANT: Cao, Yongwei
APPLICANT: Zhou, Yihua
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
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Best Local Similarity 70.7%;
Matches 302; Conservative
                                                                                         Query Match
Best Local Similarity 70.7%;
Matches 302; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Gossypium hirsutum
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Search completed: March 17, 2006, 05:35:53 Job time : 1458 secs

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(without alignments)
2440.691 Million cell updates/sec
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1 attcggctcgagtttgatcc......gaggagatttcaatcttagt 1702
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1: /cgn2_6/ptodata/1/pubpna/USOB NEW PUB.seq:*

3: /cgn2_6/ptodata/1/pubpna/USOS_NEW_PUB.seq:*

3: /cgn2_6/ptodata/1/pubpna/USOS_NEW_PUB.seq:*

4: /cgn2_6/ptodata/1/pubpna/PCT NEW_PUB.seq:*

5: /cgn2_6/ptodata/1/pubpna/PCT NEW_PUB.seq:*

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8: /cgn2_6/ptodata/1/pubpna/USOS_NEW_PUB.seq:*

9: /cgn2_6/ptodata/1/pubpna/USIS_NEW_PUB.seq:*

10: /cgn2_6/ptodata/1/pubpna/USIS_NEW_PUB.seq:*

11: /cgn2_6/ptodata/1/pubpna/USII_NEW_PUB.seq:*

12: /cgn2_6/ptodata/1/pubpna/USII_NEW_PUB.seq:*

13: /cgn2_6/ptodata/1/pubpna/USII_NEW_PUB.seq:*

13: /cgn2_6/ptodata/1/pubpna/USII_NEW_PUB.seq:*
                                                                                                                                                                   March 17, 2006, 05:11:45 ; Search time 1626 Seconds
GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    8023312 segs, 1165852854 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                                                               OM nucleic - nucleic search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                           IDENTITY NUC
Gapop 10.0 , Gapext 1.0
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Maximum DB seq length: 200000000
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                                                                                                                                                                                                                                                                                     Title:
Perfect score:
Sequence:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Sequence 523, App Sequence 25661, A Sequence 2, Appli Sequence 141, App Sequence 141, App Sequence 218, App Sequence 35, Appl Sequence 35, Appl Sequence 218, Appl Sequence 25769, A Sequence 25769, A Sequence 6, Appli Sequence 19733, A Sequence 1, Appli Sequence 2921, Ap Sequence 25, Appl Sequence 26, Appl Sequence 12913, A Sequence 364, App Description US-11-056-568A-519 US-11-052-554A-519 US-11-052-554A-519 US-11-052-554A-523 US-11-052-554A-523 US-11-052-554A-523 US-11-056-568A-25661 US-11-241-347-2 US-11-245-147-141 US-11-245-147-141 US-11-245-147-141 US-10-016-686-14 US-11-075-185-35 US-11-075-185-35 US-11-096-568A-19793 US-11-236-198-1 US-11-096-568A-25769 US-11-096-568A-10550 US-11-156-084-364 SUMMARIES Query Match Length DB 984 2000 1218 3921 1362 2954 2187 1263 7006 10968 78869 1147 42.8 42.8 43. Result No.

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Sequence 13244, A Sequence 16887, A Sequence 334, App Sequence 422, App Sequence 17358, A	Sequence 21894, A Sequence 21764, A Sequence 1616, Ap Sequence 29, Appl Sequence 29, Appl Sequence 47, Appl	Sequence 20, Appl. Sequence 22896, A Sequence 13481, A Sequence 23508, A Sequence 20321, A Sequence 26308, A Sequence 26308, A Sequence 26308, A	Sequence 20456, A Sequence 2015, Ap Sequence 1715, Ap Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli
US-11-096-568A-13244 US-11-096-568A-16887 US-11-091-883-334 US-11-091-883-422 US-11-096-568A-17358	US-11-096-568A-21894 US-09-925-065A-21764 US-11-072-512-1616 US-11-055-877-29 US-11-132-864-47	US-11-096-568A-22896 US-11-096-568A-13481 US-11-096-568A-13481 US-11-096-568A-23508 US-11-096-568A-23308 US-11-096-568A-23308	US-11-096-568A-20456 US-11-096-568A-1415 US-11-096-568A-9779 US-11-006-568A-9779 US-11-08-568A-9779 US-11-08-634A-3 US-11-086-568A-16801
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22 23 24 25	322826	1000000 100000	1 6 6 6 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4
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## ALIGNMENTS

	1,	93 109574	153	213 109455	273 ′ 109395	·
ANALOG PROBES	Length 172543; Indels 1; Gaps	CTCTCGGGCCCACGGGTCCGACCGCGATGGCAAAGACCCCGTCGTTCGCGGTGGCGGGGGGGCGTTCGCCGGGTGGCGGGGGG	CGGTCGCCGGAGGCCGGGTCGTCACAACCGGACCCAGCTCCTCCTCCTCCTCG 153	TGGCCGTCGCATCCACAGGGTTCCTCCTCCGCGGTGCCCTGCGAGACC         213	CTTGCGACGGGGGGACCCCGCCCCTCAACACCGCCGTCGCCAGGGGAGTCCCC 273	CTCCC 324
IC ACID A		ACCCCGTC	CAGCTCCT	crececee	seccercecter	CATGAGCT
PROBES AND NUCLBIC ACID ANALOG /121,086 570	6; DB 12; 0.029; ches 144;	ATGGCAAAG       GGCGCCCA	AACCGGACC         AACCGCTGC	GGGTTCCTC	CTCAACACC	crcgrcrcc
.086 D PROBES 00 11/1121,08	Score 48.6; DB Pred. No. 0.029 0; Mismatches	ccccagcgc	ccecricac      cccccccc	ATCCACAGCA         GCCGCCGCC	CCCGCCGCC	1111
on US/111210 150266459A1 TIM S. TIMETEN V. NUCLEIC ACID 18,6000-00000 NUMBER: US/1 NUMBER: 60/567 NO4-05-04 F: 107 F: 107 ersion 3.3	29%;	CACCGCGTC	GGCCGCGGG	GCCTCCGCA            'ACCGCCGCC	cereceaac     ceececea	AGGTCCAAG
086-6/c se 6, Application US/11121086 ticion No. US20050266459A1 .INFORMATION: ANT: POULSEN, TIM S. ANT: POULSEN, KIRSTEN V. OF INVENTION: NUCLEIC ACID PROBES A USFERENCE: 09138,6000-00000 TA APPLICATION NUMBER: US/11/121,086 TA PPLICATION NUMBER: 60/567,570 TY FILING DATE: 2004-05-04 APPLICATION NUMBER: 60/567,570 FILING DATE: 2004-05-04 NO 6 FILING DATE: 2004-05-04 THE: PATENTH VERSION 3.3 NO 6 HISTS: PATENTH VERSION 3.3 NO 6 HISTS: ADMAN BRANCE SEQ ID NOS: 107 HISTS: HOMO SADIENS	Similarity 50.	rccrcgggc            rcaccgggc	sercecces         seccecaaca	seccerceca         seccrccecc	rreceaceec	TCGGGTTCATGAGGTCCAAGCTCGTGCTCCTCGTCTCCCATGAGCTCTCCC
Lear Parties and the contract of the contract	atch Sal	34 CT 109633 CT	94 CC    109573 CC	154 TC 109514 CC	214 CT 109454 CT	274 TC
RESULT 1 US-11-121 Sequence GENERAL GENERAL APPLIC APPLIC TITLE TITLE CURREP CURREP PRIOR	Query Ma Best Loc Matches	& g	λ G	y S	<u>ئ</u> ۾	È

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NAME/KEY: primer bind
LOCATION: 1385..1402
OTHER INFORMATION: downstream amplification primer 99-4576 , complement
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LOCATION: 1047...1068
OTHER INFORMATION: downstream amplification primer 17-2 , complement
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DTHER INFORMATION: upstream amplification primer 99-4576
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LOCATION: 1096...1115
OTHER INFORMATION: upstream amplification primer 9-19
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LOCATION: 523..544
OTHER INFORMATION: upstream amplification primer 17-2
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LOCATION: 22324..23187
JTHER INFORMATION: homology with
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LOCATION: 1..2000
THER INFORMATION: potential
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LOCATION: 21168..21173
OTHER INFORMATION: AATAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INFORMATION: exon10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: exon
LOCATION: 19579..19752
OTHER INFORMATION: exon6
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LOCATION: 20329..20957
OTHER INFORMATION: exon9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: exon
LOCATION: 19899..19958
OTHER INFORMATION: exon7
LOCATION: 2001..2356
OTHER INFORMATION: exon1
                                                                                                                                         NAME/KEY: exon
LOCATION: 3540..3884
OTHER INFORMATION: exon2
                                                                                                                                                                                                                                                                                                                                                                                             LOCATION: 12163..12282
OTHER INFORMATION: exon3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LOCATION: 15144..15200
OTHER INFORMATION: exon4
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OTHER INFORMATION: exon5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LOCATION: 20056..20187
OTHER INFORMATION: exon8
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JOCATION: 2104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FEATURE:
NAME/KEY:
                                                                                                                                                                                                              Sequence 19793, Application US/11096568A
Publication No. US20060048240A1
GRNERAL INFORMATION:
APPLICANT: Alexandrov, Nickolai et al.
TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
TITLE OF INVENTION: Therby
TITLE OF INVENTION: Therby
CURRENT APPLICATION NUMBER: US/11/096,568A
CURRENT FILING DATE: 2005-04-01
NUMBER OF SEQ ID NOS: 34471
SEQ ID NO 19793
LENGTH: 1621
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109394 CGCTCCCAAGGAGCGCCGGCCTCGCCCTCCCGGCGTCCACGGCCGCGCGC 109344
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CCATION: (1). (1621)
OTHER INFORMATION: Ceres Seq. ID no. 12374562
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ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: exon
                                                                                                                                                    RESULT 2
US-11-096-568A-19793
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LENGTH: 23187
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LOCATION: 2563...2580
OTHER INFORMATION: downstream amplification primer 99-4557 , complement
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LOCATION: 7072...7089
OTHER INFORMATION: downstream amplification primer 99-4577 , complement
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: primer bind
LOCATION: 8576..8593
OTHER INFORMATION: downstream amplification primer 99-4559 , complement
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               complement
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OTHER INFORMATION: upstream amplification primer 99-14419 , complement
                                                                                                                                                  NAME/KEY: primer bind
LOCATION: 2074..2093
OTHER INFORMATION: downstream amplification primer 9-20 , complement
OTHER INFORMATION: downstream amplification primer 9-19 , complement
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: primer bind
LOCATION: 3882..3901
OTHER INFORMATION: downstream amplification primer 9-3 , complement
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: primer bind
COCATION: 2470..2489
JTHER INFORMATION: upstream amplification primer 9-21 , complement
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LOCATION: 4444...4463
OTHER INFORMATION: downstream amplification primer 99-14419
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LOCATION: 4336..4356
OTHER INFORMATION: downstream amplification primer 99-4558
                                                                                                                                                                                                                                               NAME/KEY: primer bind
LOCATION: 2036..2053
OTHER INFORMATION: upstream amplification primer 99-4557
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LOCATION: 3775..3792
OTHER INFORMATION: upstream amplification primer 99-4558
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LOCATION: 6638..6655
OTHER INFORMATION: upstream amplification primer 99-4577
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LOCATION: 7995..8012
OTHER INFORMATION: upstream amplification primer 99-4559
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: primer bind
LOCATION: 2483..2500
OTHER INFORMATION: downstream amplification primer 9-1
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LOCATION: 2062..2081
JTHER INFORMATION: downstream amplification primer 9-21
                                             NAME/KEY: primer bind
LOCATION: 1602...1621
OTHER INFORMATION: upstream amplification primer 9-20
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COCATION: 3455..3474
OTHER INFORMATION: upstream amplification primer 9-3
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LOCATION: 2084..2102
OTHER INFORMATION: upstream amplification primer 9-1
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APPLICANT: Alexandrov, Nickolai et al.
TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
TITLE OF INVENTION: Therby
FILE REFERENCE: 2750-1592PUS2
CURRENT APPLICATION NUMBER: US/11/096,568A
CURRENT FILING DATE: 2005-04-01
NUMBER OF SEQ ID NOS: 34471
SEQ ID NO 2921
LENGTH: 1019
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          273 CTCGGGTTCATGAGGTCCAAGCTCGTCCTCCTCCCATGAGCTCTCCCTCTTGT 332
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LOCATION: 10546. 10563
OTHER INFORMATION: downstream amplification primer 99-4560 , complement
                                                                                                                                                                                                  complement
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NAME/KEY: primer bind
LOCATION: 10996. 11015
OTHER INFORMATION: upstream amplification primer 99-14411 , complement
FEATURE:
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                                                                                                                       NAME/KEY: primer bind
LOCATION: 10023.710040
OTHER INFORMATION: downstream amplification primer 99-3148 ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: primer bind
LOCATION: 10492.10512
OTHER INFORMATION: downstream amplification primer 99-14411
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NAME/KEY: primer bind
LOCATION: 9622..9639
OTHER INFORMATION: upstream amplification primer 99-3148
                                                                                                                                                                                                                       FEATURE:
NAME/KEY: primer bind
LOCATION: 9964...3981
OTHER INFORMATION: upstream amplification primer 99-4560
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LOCATION: 11972..11990
OTHER INFORMATION: upstream amplification primer 99-4561
FRATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      21567 derecegaracecedado 21584
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US-11-096-568A-2921
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Sequence 12913, Application US/11096568A
Sequence 12913, Application US/11096568A
Publication No. US20060048240A1
GENERAL INFORMATION:
APPLICANT: Alexandrov, Nickolai et al.
TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
TITLE OF INVENTION: Therby
FILE REFERENCE: 2750-1592PUS2
CURRENT APPLICATION NUMBER: US/11/096,568A
CURRENT FILING DATE: 2005-04-01
NUMBER OF SEQ ID NOS: 34471
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 45.6; DB 7; Length 687411; Pred. No. 0.44;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 1218;
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                                                                                                                                                                                                                                                               APPLICANT: David W. Morris
APPLICANT: David W. Morris
APPLICANT: Marc Malandro
TITLE OF INVENTION: Novel Compositions and Methods in Cancer
FILE REFERENCE: 529452001300
CURRENT APPLICATION NUMBER: US/10/330,773
CURRENT FILING DATE: 2002-12-27
NUMBER OF SEQ ID NOS: 981
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 45.4; DB 9; Length 1
Pred. No. 0.018;
0; Mismatches 121; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Mismatches 109;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LOCATION: (1). (1218)
OTHER INFORMATION: Ceres Seq. ID no. 14313358
                                                          Sequence 26, Application US/10330773; Publication No. US20060040262A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; IOCATION: (1)...(687411)
; OTHER INFORMATION: n = A,T,C or G
US-10-330-773-26
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Best Local Similarity 49.4%;
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Best Local Similarity 50.5%;
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ORGANISM: Homo sapiens
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LENGTH: 1218
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Sequence 519, Application US/11052554A

Sequence 519, Application US/11052554A

Sequence 519, Application US. US20050288866A1

GENERAL INFORMATION:
TITLE OF INVENTION: COMPUTATIONAL METHOD FOR IDENTIFYING ADHESIN-LIKE

TITLE OF INVENTION: COMPUTATIONAL METHOD FOR IDENTIFYING ADHESIN-LIKE

TITLE OF INVENTION: COMPUTATIONAL OF THERAPEUTIC POTENTIAL

FILE REFERENCE: 30653/40359A

CURRENT APPLICATION NUMBER: US/11/052,554A

CURRENT FILING DATE: 2005-02-07

PRIOR PILING DATE: 2004-07-20

PRIOR PILING DATE: 2004-07-20

PRIOR FILING DATE: 2004-07-20

PRIOR FILING DATE: 2004-07-20

SOFTWARE: PROPER PROPERTY PROPERT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    133 AGCTCCTCCTCCTCCTCGTGGCCGTCGCAGCCTCCGCATCCACAGCAGGGTTCCTCC 192
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 2.7%; Score 46.2; DB 9; Length 1019; Best Local Similarity 51.2%; Pred. No. 0.0094; Matches 108; Conservative 0; Mismatches 103; Indels 0
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Best Local Similarity 52.9%; Pred. No. 0.023;
Matches 99; Conservative 0; Mismatches 88;
ORGANISM: Glycine max
PEATURE:
NAME/KEY: misc feature
LOCATION: (1)...(1019)
TOTHER INFORMATION: CERES SEQ. ID no. 14309484
US-11-096-568A-2921
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TITLE OF INVESTION: PRWTS AS MODIFIERS OF THE p53 PATHWAY AND METHODS OF USE TITLE OF INVESTION: PRWTS AS MODIFIERS OF THE p53 PATHWAY AND METHODS OF USE CURRENT APPLICATION NUMBER: US/11/241,347

CURRENT FILING DATE: 2005-09-30

PRIOR PELICATION NUMBER: US 60/296,076

PRIOR FILING DATE: 2001-06-05

PRIOR PELICATION NUMBER: US 60/328,605

PRIOR PELICATION NUMBER: US 60/338,733

PRIOR PELICATION NUMBER: US 60/338,733

PRIOR PELICATION NUMBER: US 60/357,253

PRIOR PELICATION NUMBER: US 60/357,600

PRIOR PELICATION NUMBER: US 60/357,600
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                                                                                                                                                                                                                                                                                                                                                                                                  CCTCCTCCTCCTCGTCGTCGCACCTCCGCATCCACAGGATCCTCCTCCG 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      197 CGGTGCCCTGCGAGACCCTTGCGACGGCCGTGGGGACCCCGCCGCCCCTCAACACCGCCGT 256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         464 GCCGCCGCCGCCGGCCGCCTTCGACATCCGCCACGTCCCCAGGGATCCCGACGCACCGC 523
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      404 CGTGCAGGTCGACGCCGGGTCCGACGCCGCTGCCCCGCCGCCGCTGCTCGCCCGGCGNCAG
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                                                                                                                                                                                                                                                                                         GTCGTTCGCGGTGGCGGTCGCCGGAGGCCGCGGGCCGGTTCACAACCGGACCCAGCT
                                                                                                                                                                                                                                                                                                                                           344 GTCGCGCCAGTGGCACAGGTGCGCCGACGCCGTCGAGGCCGTGCTCAGGGGGGACCCCGT
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Pred. No. 0.055;
                                                                                                                                                                               Length 1362;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CGCCAGCGGGAGTCCCCTCGGGTTCATGAGGTCCAAGCTCGTG 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0.055;
86;
                                                                                                                                                                               Score 44.4; DB 9;
Pred. No. 0.036;
0; Mismatches 112;
                                                               ; LOCATION: (1). (1362)
; OTHER INFORMATION: Ceres Seq. ID no. 13492731
US-11-096-568A-25661
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Mismatches
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Publication No. US20060024665A1
GENERAL INFORMATION:
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                                                                                                                                                                                                           Best Local Similarity 49.8
Matches 111; Conservative
ORGANISM: Zea mays subsp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              96; Conservative
                         FEATURE:
NAME/KEY: misc_feature
LOCATION: (1). (1362)
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Best Local Similarity
Matches 96; Conserv
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Publication No. US20060048240A1
GENERAL INFORMATION:
APPLICAMY: Alexandrov, Nickolai et al.
TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
TITLE OF INVENTION: Therby
FILE REPERENCE: 2750-1592PUS2
CURRENT APPLICADEN: 2050-4-01
NUMBER OF SEQ ID NOS: 34471
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Sachdeva, et al.

TITLE OF INVENTION: COMPUTATIONAL METHOD FOR IDENTIFYING ADHESIN AND ADHESIN-LIKE
TITLE OF INVENTION: PROPERING OF THERAPEUTIC POTENTIAL
FILE REPERENCE: 30853/40359A
CURRENT FILING DATE: 2005-02-07
PRIOR APPLICATION NUMBER: US 60/589,227
PRIOR APPLICATION NUMBER: IN 173/DEL/2004
PRIOR APPLICATION NUMBER: IN 173/DEL/2004
PRIOR PILING DATE: 2004-07-20
PRIOR FILING DATE: 2004-07-20
PRIOR FILING DATE: 2004-07-30
PRIOR FILING DATE: 2004-07-30
PRIOR FILING PAPE: 2004-07-30
PRIOR FILING PAPE: 2004-07-30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    42 GCCCACCGCGTCCGACCGGCGATGGCAAAGACCCCCGTCGTTCGCGGTGGCGGGGGGGTCGCC 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           102 GGAGGCCGCGGGCCCGGTTCACAACCGGACCCAGCTCCTCCTCCTCCTCGTCGTCGTC 161
                                                                           446 GTCGCCGCCTTCGCCCTCATCGTCGCCGTCACGTGTTCCTCGTGCCCCAGCCCAGCCGC 505
                                                                                                                             210 GACCCTTGCGACGGCCGTGGGGACCCCGCCCTCAACACCGCCGTCGCCAGCGGGAGT 269
                                                                                                                                                                            506 grcaaggrccrcggcagcgrcrgccrcgccrrcracarggcgcgrcrrcgrcgrcgcccgcrc 565
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  162 GCAGCCTCCGCATCCACAGCAGGTTCCTCCTCCGCGGTGCCCTGCGAGACCCTTGCGAC 221
                                                                                                                                                                                                                                 270 CCCTCGGGTTCATGAGGTCCAAGCTCGTGCTCCTCGTCCCCATGAGCTCTCCCTTCTC 328
                                                                                                                                                                                                                                                                                      566 AGCGTCATCTTCGTGGTGATCAAGACCAAGAGCGCCGAGTACATGCCCTTCTCTCGCTCTC 624
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 44.6; DB 12;
Pred. No. 0.056;
0; Mismatches 109;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; TYPE: DNA; ORGANISM: Mycobacterium tuberculosis H37Rv
US-11-052-554A-523
                                                                                                                                                                                                                                                                                                                                                                                             3-11-052-554A-523/c
Sequence 523, Application US/11052554A
Publication No. US20050288866A1
GENERAL INFORMATION:
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Best Local Similarity 50.2%;
Matches 110; Conservative
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US-11-096-568A-25661
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LENGTH: 3921
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SEQ ID NO 14
LENGTH: 1263
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       218
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       159 GTCGCAGCCTCCGCATCCACAGCAGGTTCCTCCTCCGCGGTGCCCTGCGAGACCCTTGC
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                                                                                                                                                                                                                                                                                                                                           APPLICANT: Hongjin Huang

TITLE OF INVENTION: Genetic Polymorphisms Associated with
TITLE OF INVENTION: Genetic Constant Office 
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Sequence 141, Application US/11245147

GENERAL INFORMATION:

APPLICANT: GARCIA, TERESA

APPLICANT: BARON, ROLAND

APPLICANT: THEILIABER, JOACHIM

APPLICANT: THEILIABER, JOACHIM

APPLICANT: THEILIABER, JOACHIM

APPLICANT: THEILIABER, JOACHIM

APPLICANT: GENERALD, STEVEN

APPLICANT: STEVEN

APPLICANT: BUSHNELL, STEVEN

APPLICANT: REGRESS

TITLE OF INVENTION: GENES INVOLVED IN OSTEOGENESIS, AND METHODS OF USE

FILE REFERENCE: 37991-0023
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Pred. No. 0.46;
0; Mismatches 130; Indels
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CURRENT FILING DATE: 2005-10-07
                                                                                                                                                                                                                 Sequence 5048, Application US/11124367A Publication No. US20060024700A1 GENERAL INFORMATION:
APPLICANT: Michele Cargill
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 2.6%;
Best Local Similarity 48.4%;
Matches 122; Conservative (
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CG 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          69 AAGACCCCGTCGTTCGCGGTGGCGGCGGCGGGCGCGGGCCGGCCGGTTCACAACCGG 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               36 CCTCGGGCCCACCGCGTCCGACCGGCGATGGCAAAGACCCCCGTCGTTCGCGGTGGCGGCG 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OTHER INFORMATION: canine 5T4 polypeptide having the amino acid sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        859 Anécececedentada con consecuente de la Anécece de la A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 2.6%; Score 43.8; DB 9; Length 2 Best Local Similarity 48.2%; Pred. No. 0.07; Matches 123; Conservative 0; Mismatches 132; Indels
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APPLICANT: Kingsman, Susan Mary
APPLICANT: Bebbington, Christopher Robert
APPLICANT: Bebbington, Christopher Robert
APPLICANT: Blard, Fiona Margaret
APPLICANT: Blard, Fiona Margaret
APPLICANT: Myers, Kevin Alan
TITLE OF INVENTION: Antibodies
FILE REPRENCE: 674523-2012
CURRENT APPLICATION NUMBER: US/10/016,686
CURRENT PILING DATE: 2002-11-02
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Publication No. US20060014222A1
GENERAL INFORMATION:
APPLICANT: Oxford Blomedica (UK) Limited
PRIOR APPLICATION NUMBER: PCT/IB02/02211
PRIOR FILING DATE: 2002-04-05
PRIOR APPLICATION NUMBER: 60/281,400
PRIOR FILING DATE: 2001-04-05
NUMBER OF SEQ ID NOS: 246
SOFTWARE: Patentin Ver: 3.2
SEQ ID NO 141
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PRIOR FILING DATE: 2000-11-13
NUMBER OF SEQ ID NOS: 37
SOFTWARE: Patentin version 3.1
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Matches 121; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-245-147-141
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Sorangium cellulosum

TYPE: DNA ORGANISM:

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                                                                                   78 GGGCTGGGTCTCCTCGTCGCTCACCTCCTGGGCGCCCTCCGCCGCCGCCTCCACGTC 137
                                                                                                                                                                                156 GCCGTCGCAGCCTCCGCATCCACAGCAGGTTCCTCCTCCGCGGGGGCCCTGCGAGACCCT 215
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APPLICANT: Stache-Crain, Birgit
APPLICANT: Andarmani, Susan
APPLICANT: Andarmani, Susan
APPLICANT: Tang, Y. Tom
TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
FILE REFERENCE: 821A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  89 GGCGGCGGTCGCCGGAGGCCGCGGGTTCACAAACGGGACCCAGCTCCTCCTCCTCCTCCT
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Publication No. US200502664341
GENERAL INFORMATION:
APPLICANT: JULIEN, BRYAN
APPLICANT: JULIEN, BRYAN
APPLICANT: JULIEN, BRYAN
APPLICANT: PIULIN, RALPH
TITLE OF INVENTION: BLOSYNTHETIC GENE CLUSTER FOR AMBRUTICINS
FILE REFERENCE: 010099.03
CURRENT APPLICATION NUMBER: US/11/075,185
CURRENT APPLICATION NUMBER: US 60/551,103
PRIOR PILING DATE: 2004-03-08
PRIOR PILING DATE: 2004-03-08
PRIOR FILING DATE: 2004-03-08
PRIOR FILING DATE: 2004-03-08
PRIOR FILING DATE: 2004-03-08
PRIOR FILING DATE: 2004-05-04
NUMBER OF SEQ ID NOS: 61
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96 GTCGCCGGAGGCCGCGGCCGGTTCACAACCGGACCCAGCTCCTCCTCCTCCT
                                                                                                                                                                                                                                                                                                                                                       216 TGCGACGGCCGTGGGGACCCCGCCGCCTCAACACGCGCCGCCAGCGGGA
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Pred. No. 0.17;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION NUMBER: US/10/821,234
CURRENT FILING DATE: 2004-04-07
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PRIOR APPLICATION NUMBER: US 60/462,047
PRIOR FILING DATE: 2003-04-07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 218, Application US/10821234 Publication No. US20050255114A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQ ID NOS: 1704
SOFTWARE: pt SRQ_genes Version 1.0
SRQ ID NO 218
LENGTH: 7006
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Best Local Similarity 54.8%;
Matches 86; Conservative
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ORGANISM: Homo sapiens
US-10-821-234-218
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Pred. No. 0.21;
0; Mismatches 146; Indels 1;
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Job time : 1629 secs
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Best Local Similarity 49.1%;
Matches 142; Conservative
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23         551         32.4         678         2         BG464581         BG464581         BG464581         CB663112         CSJREG0TL         CB663112         OSJREG0TL         CB663111         CB663111	ALIGNMENTS  1449 bp DNA 11  ativa Express Library Ory  211  cultivar-group) cultivar-group) tase, Streptophyta, Embry  110phyta, Liliopsida; Pos  as, Oryza.  n,C., Liu,X., Su,N., Li,I  ng,X., Bao,J., Sun,D., Zi  M. and Wang,J.  criptional regulation of  abidopsis  ormatic  Genomics	Chinese Academy of Sciences, Beijing 101300, China Tel: 86-10-804881559 Fax: 86-10-80488676 Email: chenchengeenomics.org.cn Rice genomic sequence. Class: exon-trapped.  Location/Qualifiers 1.149, Source   .149; Score 1045.8; DB 10; Length 1449; Anote="Toryas astiva exon trapped genomic sequences"   Anote="Toryas exon tr
GenCore version 5.1.7  Copyright (c) 1993 - 2006 Biocceleration Ltd.  OM nucleic - nucleic search, using sw model  Run on:  March 17, 2006, 00:15:12; Search time 7103 Seconds (without alignments) 11210.983 Million cell updates/sec  Title:  US-09-938-294-2 Sequence: 1 atcogctcgagtttgatccgaggagatttcaatcttagt 1702 Sequence: 1 atcogctcgagtttgatccgaggagatttcaatcttagt 1702 Scoring table: IDENTITY NUC Gapop 10.0, Gapext 1.0 Searched: 41078325 seqs, 23393541228 residues Total number of hits satisfying chosen parameters: Minimum DB seq length: 0 Maximum DB seq length: 2000000000	ocessing: Minimum Match 0%  Maximum Match 100% Listing first 45 summaries  EST:*  EST:*  1: gb_est1:* 2: gb_est2:* 3: gb_est3:* 4: gb_hc:* 5: gb_est4:* 6: gb_est5:* 7: gb_est5:* 7: gb_est5:* 1: gb_est5:* 1: gb_est5:* 1: gb_est5:* 1: gb_est5:* 2: gb_est4:* 6: gb_est7:* 1: gb_est5:* 1: gb_est5:* 1: gb_est7:* 8: gb_est7:* 1: gb_est6:* 8: gb_est7:* 1: gb_est7:* 1: gb_gss1:* 10: gb_gss1:* 11: gb_gss3:* 11: gb_gss3:* 12: gb_gss3:* 13: gb_gss3:* 14: gb_gss3:* 15: gb_gss3:* 16: gb_gss3:* 17: gb_gss3:* 18: gb_gss3:* 18: gb_gss3:* 18: gb_gss3:* 19: gb_gss3:* 10: gb_gss3:* 10: gb_gss3:* 10: gb_gss3:* 11: gb_gss3:* 11: gb_gss3:* 12: gb_gss3:* 13: gb_gss3:* 14: gb_gss3:* 15: gb_gss3:* 16: gb_gss3:* 17: gb_gss3:* 17: gb_gss3:* 18: gb_	1045.8

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/dollivar="WAZ"
/db_xref="taxon:4577"
/tissue type="Endosperm of 7-23DAP"
/clone lib="Endosperm 3"
/note="Vector: pBluescript SK-; Site_1:
XhoI"
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Pred. No. 4.1e-220;
0; Mismatches 14;
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Dr. Joachim Messing's lab
Waksman Institute, Rutgers University
190 Frelinghuysen Rd., Piscataway, NJ 08
Tel: 732-445-3801
Fax: 732-445-5735
Email: jlai@waksman.rutgers.edu
Seq primer: T7
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1. .908
/organism="Zea mays"
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1 (Dases 1 to 908)
Lai,J., Dey,N., Kim,C.S., Bharti,A.K., Rudd,S., Mayer,K.F., Larkins,B., Becraft,P. and Messing,J.
Characterization of the maize endosperm transcriptome and its comparison to the rice genome
Comparison to the rice genome
Genome Res. 14 (10), 1932-1937 (2004) Site_2: GCCGGAGGGACCACGGAGAGATCGTCGTGGACGGCTCAACCGGCCTCCTGCACCCCCGCCGGG CTGGGGAATAGTAAAGAACTAATGGAAGTTGCTGAAGACAATGTCGCAAGAGAGTCCTA 908 CTGGGGAATAGTAAAGAACTAATGGAAGTTGCTGAAGACAATGTCGCAAGAAGAGTCTTA GCTGGAGGGACCACGGAGATCGTCCTGGACGGCTCGACTGGCCTTCTGCATCCTGCTGGG Gaps

\$1.00 ACCIDENTAL CONTRACT CONTRACT TO THE PROPERTY OF THE PROP	Anchoring 9,371 maize expressed sequence tagged unigenes to the bacterial artificial chromosome contig map by two-dimensional overgo hybridization  NAL Plant Physiol. 134 (4), 1317-1326 (2004)  RED 15020742  C (Dases 1 to 843)  RAINILLI, M., Hanafey, M., Morgante, M. and Tingey, S.V.  Arthur, L.W., Hanafey, M., Morgante, M. and Tingey, S.V.  Maize Mapping Project/DuPont Consensus Sequences for Design of Overgo Probes  Overgo Probes  NAL Unpublished (2002)  S (Dases 1 to 843)  RS Coo, E.H.  Direct Submission  S Direct Submission  S Lobert Submission  S Lobert Submission  S Like S Lobert Submission  If you are interested in getting corresponding physical clones, these are publicly available from ZnDB and may be found by Blass Hearthing at MST, maizeman ord; ZnDB, www. Zndb, isrtate.edu: TIGR.	s urce	/ Match Similarity 99.2%; Pred. No. 6.1e-219; Local Similarity 99.2%; Pred. No. 6.1e-219; Pred. No. 6.1e-219; Local Similarity 99.2%; Pred. No. 6.1e-219; Pred. No. 6.1e-2	139   TCCTCCTCCTCGTGGCCGTCGCATCCACAGCAGGGTTCCTCCTCCGCG   198
846 CGGGAACATATTCGTGAATCCC-TGGAGTTCGAGGATTCCAGGTTTGCAATTATTCCAGGATTTGCAATTATTCGTGAATTTTCCAGGATTTTGCTGAATTTTTCCAGGATTTTTCCAGGATTTTTTCCAGGATTTTTCCAGGATTTTTCCAGGATTTTTCCAGGATTTTTTCCAGGATTTTTTTCCAGGATTTTTTCCAGGATTTTTTCCAGGATTTTTTTCCAGGATTTTTTTCCAGGATTTTTTTCCAGGATTTTTTTCCAGGATTTTTTTT	JOURL POURL PUBERERE AUTH TITLI JOURL REFERE AUTH TITLI JOURL	FEATURI		8 8 8 8 8 8 8 8 8 8
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selection of mRNA with a 5' cap. After synthesis of cDNA, a normalization step was conducted against the mixture of RNA sources. Tissues prepared: 1. just emerging silks; 2. inner husks from ears of sample #1; 3. 20 dap aleurone; 4. immature tassels, stages from 1-2 mm to 1-2 cm; 5. 2 mm to 2 cm ears; 6. pollen; 7. 1 cm vegetative shoot tips from 15 day old seedlings; all leaves with an expanded or partially expanded sheath were removed; 8. mature leaf tissue; 9. 0.5 cm long root tips from 15 day old seedlings; 10. 10 dap whole seed; 11. 12 dap endosperm and embryo; 12. 17 dap endosperm and embryo. All 16 the sequenced clones in Maize Full-length cDNA Project will be archived at the University of Arizona. Clones, high density filters and amplified library can be ordered from the University of Arizona. edu/orders/)."	Query Match         44.3%;         Score 753.8;         DB 8;         Length 758;           Best Local Similarity         99.6%;         Pred. No. 1.6e-201;           Matches 755;         Conservative         0;         Mismatches         3;         Indels         0;         Gaps         0;           Qy         30         GTCTCTCTCTCGGGCCGCGCGCGCGGCAAAGACCCGTCGTCGTCGTGGGGGG         89         0;         0;         0;         0;         0;         0;         0;         0;         0;         0;         0;         0;         0;         0;         0;         0;         0;         0;         0;         0;         0;         0;         0;         0;         0;         0;         0;         0;         0;         0;         0;         0;         0;         0;         0;         0;         0;         0;         0;         0;         0;         0;         0;         0;         0;         0;         0;         0;         0;         0;         0;         0;         0;         0;         0;         0;         0;         0;         0;         0;         0;         0;         0;         0;         0;         0;         0;         0;         0;         0;	0   0   0   0   0   0   0   0   0   0
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572 TGAAGAACACGATTCATGACCGTGTCCATTTTGTGAACAAGACATTGGCAGTGGCCCCTT

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512 ACTIGGGAGCAATTGATGATGGCTTGTTCAGAATTCTCAGGGCCCTGGGAATGCTTTGGAA

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/tissue_type="mixed (silks, husks, ears, pollen, shoot
tips, leaf, root tips, whole seed, embryo)"
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/dev stage="varies by tissue"
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NotI; Maize Full length cDNA library (3530 library)
created by Invitrogen from multiple tissues; Organ: silks,
husks, ears, pollen, shoot tips, leaf, root tips, whole
seed, embryo. This is a Gateway compatible vector,
permitting clone movement to new vector backbones for
expression in diverse host cells using recombination
rather than restriction enzymes. poly(A)+ mRNA was
prepared by Invitrogen, and equimolar amounts of RNA from
each of the 12 tissue samples were mixed together for
selection of mRNA with a 5' cap. After synthesis of cDNA,
a normalization step was conducted against the mixture of
RNA sources. Tissues prepared: 1. just emerging silks; 2.
inner husks from ears of sample #1; 3. 20 dap aleurone; 4.
innature tassels, stages from 1-2 mm to 1-2 cm; 5. 2 mm to
2 cm ears; 6. pollen; 7. 1 cm vegetative shoot tips from
partially expanded sheath were removed; 8. mature leaf
tissue; 9. 0.5 cm long root tips from 15 day old seedlings; 10. 10 dap whole seed; 11. 12 dap endosperm and
embryo; 12. 17 dap endosperm and embryo; All length con the seed in Maize Full-length cDNA Project will be
archived at the University of Arizona. Clones, high
density of files and amplified library can be ordered from
                                                                                                                                                                                                                           Edwaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnollophyta; Liliopsida; Poales; PacCAD clade; Panicoideae; Andropogoneae; Zea.

E 1 (bases 1 to 752)
S Kim.H., Collura,K., Wissotski,M., Smart,D., Kudrna,D., Muller,C., Maice Full-length CNA Project
Maize Full-length CNA Project
Unpublished (2005)
Contact: Yeisoo Yu Arizona Genomics Institute
The University of Arizona
Forbes Building Room 303, Tucson, AZ 85721-0036, USA
Tel: 520 621 1259
                                                                  790488 11near EST 27-JUL-2005 BFb0009H19.f ZM_BFb Zea mays CDNA 3', mRNA sequence.
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(http://www.genome.arizona.edu/orders/)."
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Plate: 0009 row: H column: 19.
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                                                                                                                                     GI:71308499
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AUTHORS
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EST 28-JUL-2005 Zea mays

Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Bukaryota, Magnoliophyta, Liliopsida, Poales, Poaceae, PACCAD
clade, Panicoideae, Andropogoneae, Zea.
1 (bases I to 73.)
Kim, H., Collura, K., Wissotski, M., Smart, D., Kudrna, D., Muller, C.,
Rao, K., Haller, K., Wing, R., Soderlund, C., Walbot, V. and Yu, Y.
Maize Full-length, CDNA Project
Unpublished (2005) ZM_BFD0030M17.r ZM_BFD Zea mays cDNA 5', mRNA sequence. DR805336
DR805336.1 GI:71421195 Contact: Yelsoo Yu Arizona Genomics Institute The University of Arizona Forbes Building Room 303, Tucson, AZ 85721-0036, USA Tal: 520 625 9585 Fax: 520 621 1259 2еа шаув EST ACCESSION VERSION KEYWORDS SOURCE ORGANISM DEFINITION TITLE JOURNAL COMMENT REFERENCE AUTHORS RESULT 6 DR805336

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Gaps ö 886 TTGCAATAATAAACAGTGTATCACGAGGAAAGGGACAAGACTTATTTCTTCAAGCATTTT 945 

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al Similarity 100.0%; Pred. No. 5.3e-201;
752; Conservative 0; Mismatches 0; Indels

Query Match Best Local Similarity Matches 752; Conserv

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ZM BFD0026K16.f ZM_BFD Zea mays cDNA 3', mRNA sequence.
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DR802415.1 GI:71331163
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(Dases 1 to 730)

Kim,H., Collura,K., Wissotski,M., Smart,D., Kudrna,D., Muller,C., Rac,K., Haller,K., Wing,R., Soderlund,C., Walbot,V. and Yu,Y.

Maize Full-length cDNA Project
Unpublished (2005)
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                           481 AAGCTGATCTGGTTATCTTAAACACTGCTGTTGCTGGCAAGTGGCTTGACCCTGTTCTGA
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Arizona Genomics Institute
The University of Arizona
Forbes Building Room 303, Tucson, AZ 85721-0036, USA
Tel: 520 626 9585
Fax: 520 621 1259
Fax: 120 621 1259
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/dev stage="waries by tissue"
/lab host="DH10B TI phage resistant"
/clone lib="ZM_BFb"
/clone lib="ZM_BFb"
/note="Vector: pCWV-SPORT 6.1; Site 1: BCGRV; Site 2:
/note="Westor: pCWV-SPORT 6.1; Site 1: BCGRV; Site 2:
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yeisoo@genome.arizona.edu
                                         30 row: M column: 17. Location/Qualifiers
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                                                                                                                                                                            organism="Zea mays"
                                                                                                                                                                                                                 /mol_type="mRNA"
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RNA sources. Tissues prepared: 1. just emerging silks; 2. inner husks from ears of sample #1; 3. 20 dap aleurone; 4. immature tassels, stages from 1-2 mm to 1-2 cm; 5. 2 mm to 2 cm ears; 6. pollen; 7. 1 cm vegetative shoot tips from 15 day old seedlings; all leaves with an expanded or partially expanded sheath were removed; 8. mature leaf tissue; 9. 0.5 cm long root tips from 15 day old seedlings; 10. 10 dap whole seed; 11. 12 dap endosperm and embryo; 12. 17 dap endosperm and embryo; 12. 17 dap endosperm and embryo; 12. 17 dap endosperm and embryo; 12. 19 day endosperm and embryo; 12. 10 day whole seed; 11. 12 dap endosperm and embryo; 12. 17 day endosperm and embryo; 13. 19 day endosperm and embryo; 12. 19 day endosperm and embryo; 13. 19 day endosperm and embryo; 14. 19 day endosperm and embryo; 15. 19 day endosperm end
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         886 TTGCAATAATAAACAGTGTATCACGAGGAAAAGGGACAAGACTTATTTCTTCAAGCATTTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 tch 42.9%; Score 730; DB 8; Le sal Similarity 100.0%; Pred. No. 8.8e-195; 730; Conservative 0; Mismatches 0;
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Best Local Similarity
Matches 730; Conserv
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rather than restriction enzymes. poly(A)+ mRNA was prepared by Invitrogen, and equimolar amounts of RNA from each of the 12 tissue samples were mixed together for selection of mRNA with a 5' cap. After synthesis of cDNA, a normalization step was conducted against the mixture of RNA sources. Tissues prepared! . just emerging silks; 2. inner husks from ears of sample #1; 3. 20 dap aleurone; 4. immature tassels, stages from 1-2 mm to 1-2 cm; 5. 2 mm to 2 cm ears; 6. pollen; 7. 1 cm vegetative shoot tips from 15 day old seedlings; all leaves with an expanded or partially expanded sheath were removed; 8 mature leaf tissue; 9. 0.5 cm long root tips from 15 day old eedlings; 10. 10 day whole seed; 11. 12 dap endosperm and embryo; 12. 17 dap endosperm and embryo. All of the sequenced clones in Maize Full-length cDNA Project will be archived at the University of Arizona. Clones, high the University of Arizona.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /db xref="taxon:4577"
/tissue_type="mixed (silks, husks, ears, pollen, shoot
tips, laff, root tips, whole seed, embryo]"
/dev stage="varies by tissue"
/dab_host="bH10B T1 phage resistant"
/clone lib="XM BFb"
/note="Vector: pCMV-SPORT 6.1; Site_1: EcoRV; Site_2:
/note="Vector: pCMV-SPORT 6.1; Site_1: EcoRV; Site_2:
/note="Vector: pCMV-SPORT 6.1; Site_1: EcoRV; Site_2:
/note; Maize Fnll length cDNA library (3530 library)
created by Invitrogen from multiple tissues; Organ: silks,
husks, ears, pollen, shoot tips, leaf, root tips, whole
seed, embryo. This is a dateway compatible vector,
permitting clone movement to new vector backbones for
expression in diverse host cells using recombination
-the content of the content of
                                          EST 27-JUL-2005
                                                                                                                                                                                                                                                                                                                                                Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, PACCAD
clade, Panicoldeae, Andropogoneae, Zea.
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Kim, H., Collura, K., Wissotski, M., Smart, D., Kudrna, D., Muller, C.,
Kao, K., Haller, K., Wing, R., Soderlund, C., Walbot, V. and Yu, Y.
Maize Full-length cDNA Project
Unpublished (2005)
Contact: Yeisoo Yu
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                                              DR790489 11near ES:
ZM EFb0009H19.r ZM_BFb Zea mays CDNA 5', mRNA sequence
DR790489
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The University of Arizona
Forbes Buliding Room 303, Tucson, AZ 85721-0036, USA
TTE: 520 625 9585
Fax: 520 621 1259
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bmail: yeisoo@genome.arizona.edu
Plate: 0009 row: H column: 19.
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/mol_type="mRNA"
/cultivar="B73"
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Matches 711; Conservative
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Zea mays
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DR790489
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AUTHORS
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CA184773 8T3 Saccharum officinarum CDNA clone SCSBST3093D01 5', mRNA sequence.
CA184773.1 GI:35122872
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                                                                                                                                                                                                                                                                                             9
                                      /cell type="embryo sac" /clone lib-"Zea mays embryo sac cDNA library" /clone lib-"Zea mays embryo sac cDNA library" /note="Vector: Clontech Triplex2; Embryo sacs were isolated with enzymatic maceration and manual microdissection. RNA was extracted from the embryo sacs cDNA library was constructed by oligo dT priming using clontech SNART cDNA synthesis kit. The cDNAs were directionally cloned."
                                                                                                                                                                                                                                                                                                                                                         61 AACACGAGAAACTTAAAGTGCCTAGAATACATGCTGTGGTGGGGAAGTGATGTTAATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        241 TIGITICAGAATICTCAGGGCCGTGGAGAATGCTTTGGAAGATACAATTGAACCAATGG
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                                                                                                                                                                                                                                                                                                                           AACACGAGAAACTTAAAGTGCCTAGAATACATGCTGTAGTTGTGGGAAGTGATGTTAATG
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                                                                                                                                                                                                    Length 676;
                                                                                                                                                                                                                                5; Indels
                                                                                                                                                                                                 Score 667; DB 8; I
Pred. No. 5.9e-177;
0; Mismatches 5;
           /db_xref="taxon:4577"
/clone="ES13236"
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Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD

clade; Panicoideae; Andropogoneae; Zea.

(bases 1 to 676)

Yang, H. and McCormick, S.

Transcriptome of Zea mays embryo sac
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TCGCCCGGAGGCCGCGGGCCCGGTTCACAACCGGACCCAGCTCCTCCTCCTCCTCCTCGTGG
                                                              CGTCGCAGCCTCCGCATCCACAGCAGGTTCCTCCTCCGCGGTGCCCTGCGAGACCCTT
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                                                                                                             GCGACGGCCGTGGGGACCCCGCCGCCCTCAACACCGCCGTCGCCAGCGGGAGTCCCCTCG
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800 Buchanan St. Albany, CA 94710,
810 Buchanan St. Albany, CA 94710,
Fax: 510 559 5678
Email: shailamc@nature.berkeley.edu
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Contact: Yang, H.; McCormick,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Zea mays"
/mol_type="mRNA"
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Lugaration, Gowda, M., Haller, K., Hatfield, J., Lu, G., Stahlberg, B., Zhou, B., Li, H., Kim, H., Yu, Y., Dean, R.A., Wing, R.A., Soderlund, C. and Wang, G.L. Large-scale identification of expressed sequence tags involved in
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Oryza sativa (japonica cultivar-group)
Eukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.

1 (bases 1 to 831)
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OSJNEG04009.f OSJNEd Oryza sativa (japonica cultivar-group) cDNA clone OSJNEG04009 5', mRNA sequence.
ATATAGCTTGGAGCATAGGATGTTGAACCATGGAGGTGCAGGTTTTACCAGTTAGGGGACA
                                                                                                                                                                                                  GGAGGCAGTIGATATIGCTCTGAAAGCTGATCTGGTTATTNTAAACACTGCTGTTIGCTTG
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/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nipponbare"
/db_xref="taxon:39947"
/clone="OSJNEG04009"
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Biological Sciences West, 448A, P.O. Box 210088, Tucson, AZ
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Plant Physiol. 138 (1), 105-115 (2005)
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BACKWARD: gga aac agc tat gac cat g
Plate: 04 row: O column: 09
Seq primer: gta aaa cga cgg cca gtg.
Location/Qualifiers
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Tel: 520 626 3967
Fax: 520 621 9288
Email: rwing@genome.arizona.edu
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/clone_lib="ST3"
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/clone_lib="ST3"
/clone_lib="State_l: Sali, Site_l: Not1; An unidixectional cDNA library generated from [Fourth apical stalk internodes of adult plants]. CDNA was prepared from polyA+ mRNA using SuperScript Plasmid System Kit (Invitrogen). The double-strand cDNAs were fractionated in a sepharose CL-2B 40cm-columns and fragments sizing between 0.8 and 1.5 KD were directionally cloned into the vector. Details of each source of RNA and library construction can be obtained at http://sucest.lad.ic.unicamp.br/public"
                                                                      Bukaryota, Viridiplantae, Streptophyta; Embryophyta, Tracheophyta,
Spermatophyta; Magnoliophyta; Liliopsida, Poales, Poaceae, PACCAD
clade, Panicoideae, Andropogoneae; Saccharum, Saccharum officinarum
                                                                                                                                                                              Vettore, A. L., das Silva, F. R., Kemper, E. L. and Arruda, P.

The libraries that made SUCEST
Genet. Mol. Biol. 24 (1-4), 1-7 (2001)
Genter. Arruda P
Contact: Arruda P
Contro de Biologia Molecular e Engenharia Genetica
Universidade Estadual de Campinas
Gaixa Postal 6010, 13083-970, Campinas SP, Brazil
Tel: 55 19 3788 1137
Fax: 55 19 3788 1137
Fax: 55 19 3788 1137
Clone distribution: clone distribution information can be found through the Brazilian Clone Gollection Center (BCCC) at http://www.bcccenter.fcav.unesp.br
Plate: 033 row: D column: 01
Seq primer: T7 Promoter Primer.
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Pred. No. 9.2e-175;
0; Mismatches 64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       organism="Saccharum officinarum"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /mol_type="mRNA"
/db_xref="taxon:4547"
/clone="SCSBST3093D01"
                                                  Saccharum officinarum
                             Saccharum officinarum
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llarity 91.4%;
Conservative
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Best Local Si
Matches 731;
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 /tissue_type="Leaf"
/dev_stage="3 week"
/lab_host="DH108"
/clone_lib="OSJNEd"
/note="Vector: pBluescript II KS +; Site_1: EcoRI; Site_2:
XhoI; 24 hrs after innoculation with Rice_Blast (C9240-Ī)"
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                                                                                                                                                                                                                                                                                                          243 ATTACCTGCTAGGGGACATGAGGCGATTGATACTGCCCTAAAGGCTGATCTTGTTATCTT
                                                                                                                                                                                                                                                                                                                                       536 AAACACTGCTGTTGCTGGCAAGTGGCTTGACCCTGTTCTGAAAGATCATGTTCCTAAAGT
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                                                                                                                                                                    CGTGCTCCTCGTCTCCCATGAGCTCTCCCCTCTGGTGGTCCCACTTTTACTGAAGTT
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                                                                                   Length 831;
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                                                                                  Query Match 38.6%; Score 656.8; DB 6; Best Local Similarity 87.0%; Pred. No. 4.9e-174; Matches 721; Conservative 0; Mismatches 108;
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CD435900 675 bp mRNA linear BST 03-JUN-2003 EL01N0367F09.b Endosperm_3 Zea mays cDNA, mRNA sequence.

RESULT 12 CD435900 LOCUS DEFINITION

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TGACTTTGTGGTGAAGAACACGATTCATGACCGTGTCCATTTTGTGAACAAGACATTGGC 1114
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                                                                                      Eukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogonae; Zea.

1 (Janicoideae; Andropogonae; Zea.

1 (Janes 1 to 675)

Lai, J., Dey, N., Kim, C.S., Bharti, A.K., Rudd, S., Mayer, K.F., Larkins, B., Becraft, P. and Messing, J.

Comparison to the maize endosperm transcriptome and its comparison to the rice genome

Genome Res. 14 (10), 1932-1937 (2004)
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/mol_type="mRNA"
/cultivar="W22"
/db_xref="taxon:4577"
/tissue_type="Endosperm of 7-23DAP"
/clone_lib="Endosperm_3"
/note="Vector: pBluescript SK-; Site_1: EcoRI; %
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Pred. No. 3.4e-172;
0; Mismatches 3;
                                                                                                                                                                                                                                                                                        Contact: Lai, Jinsheng
Dr. Joachim Messing's lab
Mscman Institute, Rutgers University
190 Frelinghuysen Rd., Piscataway, NJ
Tel: 732-445-3801
Email: jlai@waksman.rutgers.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
                    GI:31351543
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Best Local Similarity 99.4%;
Matches 663; Conservative
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CD435900
CD435900.1
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Zea mays
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	718 GGAATAGCAGACTAGCGATCGCCTGAAAATACCAGATGCCACAAACTTATGTTCACC		QY         1138 TTGATGTGCTTGTTCAGAATTCTCAGGGCGGGGGAATGCTTTGGAAGGATAACAATTG           DD         721 CTGATGTGCTTGTTCAGAACTCTCACGCCGTGGAGAATGCTTTGGAAGGATAACGATTG           QY         1198 AAGCAATGGCATTCAAGTTGCCAGTATTGGGCA           120	VERSION VERSION VERSION VERNING VERNING SOURCE Soa mays ORGANISM Zea mays Clade; Panicoldeae; Andropogoneae; Zea.  REFERENCE I (bases 1 to 753) AUTHORS Verza,N.C., Silva,T.R., Cord-Neto,G., Noqueira,F.T.S., Fisch,P.H., De Rosa,V.E. Jr., Martins,M.M., Vettore,A.L., da Silva,F.R. and Arruda,P.  TITLE Arruda,P. TITLE Transcriptome-wide analysis of expressed sequence tags COMMENT CONTRAL
Db 489 TGACTTTGTGGTGAAGAACACGATTCATGACCGTGTCCATTTTGTGAACAAGACATTGC 548  Qy 1115 AGTGGCCCTTACTTGGCAGCAATTGATGTGTTTTTCAGAATTCTCAGGGCCGTGGAGA 1174	CB660163 CB660163 CB660163 LOCUS CB660163 LOCUS CB660163 CBFINITION OSJNEG01K22.f OSJNEd Oryza sativa (japonica cultivar-group) cDNA CLOCUS ACCESSION CB660163.1 GI:29663888 KEYWORDS CB660163.1 GI:29663888 CWERSTON CCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC	REFERENCE Biniartoideae; Oryzae.  Biniartoideae; Oryzae.  AUTHORS Jantasuriyarat, C., Gowda, M., Haller, K., Hatfield, J., Lu, G., Stahlberg, E., Zhou, B., Li, H., Kim, H., Yu, Y., Dean, R.A., Wing, R.A., Soderlund, C. and Wang, G.L.  TITLE Large-scale identification of expressed sequence tags involved in JOURNAL Plant Physiol. 138 (1), 105-115 (2005)  PUBMED 15888683  COMMENT Contact: Rod Wing Arizona Genomics Institute University of Arizona Biological Sciences West, 448A, P.O. Box 210088, Tucson, AZ B5721-0088, USA Tel: 520 626 3967	EAX: 520 621 9288 Email: rwing@genome.arizona.edu PCR PRimers FORWARD: gta aaa cga ccg gtg BACKWARD: gga aac agc cat gg Plate: 01 row: K column: 22 Seq primer: gta aaa cga cgg cca gtg.  FEATURES I813 / mol type="mRNA" / mol type="mRNA" / clone="OSJNEGOIK2" / tiseu: type="Leaf" / dev stace="leaf" / dev stace="leaf"	/lab_nost="Display="The content of the content of t

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Zea mays
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//clone lld="Organ: seedy Vector: pSPORTI; Site 1: Sall; Site 2:
Not1; Plant Material and RNA Isolation: Fleld grown maize plants from inbred line F352 were used Ears were plants from inbred line F352 were used. Ears were harvested at 10, 15, 20 and 25 days after pollination (DAP), seeds were cut from the ear and the upper third of the endosperms, containing only endosperm, aleurone and pericarpal tissues, was removed, frozen in liquid nitrogen and stored at -800 C. Frozen endosperms were pulverized in liquid nitrogen and total RNA was isolated according the method of Manning (9). Poly(A) +RNA was isolated using Oligotex-dT. CDNA libraries were constructed using SuperScript Plasmid System for CDNA Synthesis and Plasmid Cloning Kit as described in Vettore, et al., (2001) The libraries that made SUCEST. Genet Mol Biol 24: 1-7. CDNAs ranging from 500 to 800 bp in size were assigned as short libraries (S10, S15, S20), and CDNAs S800 were assigned as long libraries (S10, S15, S20), and CDNAs S00 were assigned as long libraries (LD, L15, M15, M15, L20, L25). Unamplified transferred to 96 well plates containing liquid Circle Grow (CG) medium supplemented with 100 mg/L of ampicillin and 8% glycerol. Three copies of each CDNA clone were stored at -800 c. Additional information can be found in: Verza, N.C., Silva, T.R., Cord-Neto, G., Nogueira, F.T.S, Fisch, P.H., De Ross Jr., V.E., Martins, M.M., Vettore, A.L., da Silva, F.R. and Arruda, P. (2005)
Endosperm-preferred expression of maize genes as revealed by transcriptome-wide analysis of expressed sequence tags.
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                                                                                                                                                                                                                                                                                                                 /tissue_type="endosperm"
/dev stage="multiple stages (10 to 25 days after
/dev stage="multiple stages (10 to 25 days after
/dev stage="multiple stages (10 to 25 days after
/dev stage="multiple"
/lab host="E. coli DH10B"
/clone_lib="Maize Endosperm cDNA Library"
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Centro de Biologia Molecular e Engenharia Genetica
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                 Universidade Estadual de Campinas
Caixa Postal 6010, 13083-970, Campinas SP, Brazil
Tel: 55 19 3788 1137
Exax: 55 19 3788 1089
Email: parruda@unicamp.br.
Location/Qualifiers
                                                                                                                                                                                                               /mol_type="mRNA"
/cultivar="F-352 near isogenic line"
/db_xref="taxon:4577"
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                                                                                                                                                                                                                                                                                               /sex="hermaphrodite"
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/tissue types"mixed (silks, husks, ears, pollen, shoot
tips, leaf, root tips, whole seed, embryo"
/dev stage="waries by tissue"
/dev stage="waries by tissue"
/lab host="DH10B II phage resistant"
/clone_lib="ZM_BFb"
/clone multiple tissues; Organ: silks,
husks, ears, pollen, shoot tips, leaf, root tips, whole
seed, embryo. This is a Gateway compatible vector,
permitting clone movement to new vector backbones for
expression in diverse host cells using recombination
rather than restriction enzymes. poly(A) + mRNA was
prepared by Invitrogen, and equimolar amounts of RNA from
                                                                                                            1372
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoldeae; Andropogoneae; Zea.

1 (Dases 1 to 629)

Kim,H., Collura,K., Wissotski,M., Smart,D., Kudrna,D., Muller,C., Maize,K., Haller,K., Wing,R., Soderlund,C., Walbot,V. and Yu,Y.

Unpublished (2005)
389 TCTTGCAAAGAACATCGTCAGACTCGCAAGCCACGCCGAGCAGAGAGTCTCCATGGGGGA
                                                                                                                                                                                                                                                                                                          449 AAAGGGCTATGGCAGGCTGAAAGGAAATGTTCATGGAGCACCACATGGCTGAGAGGATCGC
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                                                                                                            1313 TCTTGCAAAGAACATCGTCAGACTCGCAAGCCACGCCGAGCAGGGGTCTCCATGGGGGA
                                                                                                                                                                                                                                              1373 AAAGGGCTATGGCAGGGTGAAGGAAATGTTCATGGAGCACCACATGGCTGAGAGGATCGC
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DR805335.1 GI:71421191
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Fax: 520 621 1259
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Location/Qualifiers
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The University of Arizona
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/cultivar="B73"
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selection of mRNA with a 5' cap. After synthesis of CDNA, a normalization step was conducted against the mixture of RNA sources. Tissues prepared: 1. just emerging silks; 2. inner husks from ears of sample #1; 3. 20 dap aleurons; 4. immature tassels, stages from 1-2 mm to 1-2 cm, 5. 2 mm to 2 cm ears; 6. pollen; 7. 1 cm vegetative shoot tips from 15 day old seedlings; all leaves with an expanded or partially expanded sheath were removed; 8. mature leaf tissue; 9. 0.5 cm long root tips from 15 day old seedlings; 10. 10 dap whole seed; 11. 12 dap endosperm and embryo; 12. 17 dap endosperm and embryo. All of the sequenced clones in Maize Full-length cDNA Project will be archived at the University of Arizona. Clones, high density filters and amplified library can be ordered from the University of Arizona.
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